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<120> CLASP-5 Transmembrane Protein

<130> 020054-000511US

<140> US 09/736,960

<141> 2000-12-13

<150> US 60/160,860

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<170> PatentIn Ver. 2.1

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Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser	
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 His Val Arg Asp Cys Val Gln Thr Tyr Ile Arg Glu Trp Leu Ile Val
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 Gly Ser Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu
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 Ser Glu Thr Leu Glu Cys Ser Glu Pro Ala Ala Gln Ala Gly Pro Arg
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 His Leu Asn Val Leu Cys Asp Val Ser Gly Lys Gly Pro Val Thr Ala
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 Cys Asp Phe Asp Leu Arg Ser Leu Gln Pro Asp Lys Arg Leu Glu Asn
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Val Asp Glu Ser Arg Ala Val Glu Ile Asp Leu Val Leu Glu Lys Thr
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Lys Glu His Leu Gly Asn Arg Ile Leu Val Lys Leu Leu Thr Leu Lys
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 Phe Glu Ile Glu Ile Glu Pro Leu Phe Ala Ser Ile Ala Leu Tyr Asp
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 Val Lys Glu Arg Lys Lys Ile Ser Glu Asn Phe His Cys Asp Leu Asn
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 Ser Asp Gln Phe Lys Gly Phe Leu Arg Ala His Thr Pro Ser Val Ala
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 Ala Ser Ser Gln Ala Arg Ser Ala Val Phe Ser Val Thr Tyr Pro Ser
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 Ser Asp Ile Tyr Leu Val Val Lys Ile Glu Lys Val Leu Gln Gln Gly
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 Phe Lys Phe Leu Ala Asp Tyr Lys Arg Ser Ser Ser Leu Gln Arg Arg
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 Val Lys Ser Ile Pro Gly Leu Leu Arg Leu Glu Ile Ser Thr Ala Pro
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 Phe Pro Glu Asn Arg Thr Arg Pro His Lys Glu Ile Leu Glu Phe Pro
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Glu	Val	Tyr	Thr	Ala	Val	Thr	Tyr	His	Asn	Lys	Ser	Pro	Asp	Phe	Tyr
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Glu	Glu	Val	Lys	Ile	Lys	Leu	Pro	Ala	Lys	Leu	Thr	Val	Asn	His	His
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Leu	Leu	Phe	Thr	Phe	Tyr	His	Ile	Ser	Cys	Gln	Gln	Lys	Gln	Gly	Ala
			580					585					590		
Ser	Val	Glu	Thr	Leu	Leu	Gly	Tyr	Ser	Trp	Leu	Pro	Ile	Leu	Leu	Asn
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Glu	Val	Gln	Ala	Val	Ser	Ser	Val	His	Thr	Gln	Asp	Asn	His	Leu	Glu
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Lys	Phe	Phe	Thr	Leu	Cys	His	Ser	Leu	Glu	Ser	Gln	Val	Thr	Phe	Pro
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Ile	Arg	Val	Leu	Asp	Gln	Lys	Ile	Ser	Glu	Met	Ala	Leu	Glu	His	Glu
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Leu	Lys	Leu	Ser	Ile	Ile	Cys	Leu	Asn	Ser	Ser	Arg	Leu	Glu	Pro	Leu
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Val	Leu	Phe	Leu	His	Leu	Val	Leu	Asp	Lys	Leu	Phe	Gln	Leu	Ser	Val
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Gln	Pro	Met	Val	Ile	Ala	Gly	Gln	Thr	Ala	Asn	Phe	Ser	Gln	Phe	Ala
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Phe	Glu	Ser	Val	Val	Ala	Ile	Ala	Asn	Ser	Leu	His	Asn	Ser	Lys	Asp
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His	Tyr	Val	Phe	Arg	Leu	Pro	Glu	Val	Gln	Arg	Asp	Val	Pro	Lys	Ser
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850 855 860

Ser Arg Met Ser Tyr Tyr Cys Ser Gly Ser Ser Asp Ala Pro Ser Ser
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Pro Ala Ala Pro Arg Pro Ala Ser Lys Lys His Phe His Glu Glu Leu
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Ser Gln Leu Ser Ala Lys Leu Ser Asn Leu Pro Thr Leu Ile Ser Met
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Arg Leu Glu Phe Leu Arg Ile Leu Cys Ser His Glu His Tyr Leu Asn
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Leu Asn Leu Phe Phe Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys
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Pro Ser Ile Ser Ser Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp
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Gln Lys Ile Ala Ser Met Phe Asp Leu Thr Ser Glu Tyr Arg Gln Gln
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His Phe Leu Thr Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp
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Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu
1665 1670 1675 1680

Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp
1685 1690 1695

Ser Ile Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg
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Val Gly Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe
1715 1720 1725

Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg
1730 1735 1740

Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val
1745 1750 1755 1760

Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg
1795 1800 1805

Phe Met Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu
1810 1815 1820

Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala
1825 1830 1835 1840

Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe
1845 1850 1855

Val Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr
1860 1865 1870

Leu Gln Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met
1875 1880 1885

Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly
1890 1895 1900

Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro
1905 1910 1915 1920

Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe
1925 1930 1935

Ile Met Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr
1940 1945 1950

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1955 1960 1965

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Ser Pro Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu	
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Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu	
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Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile	
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Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala Thr Ser	
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Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg	
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Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp Ser Ile	
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Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu Met Lys	
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Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys	
930 935 940	
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Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys	
945 950 955	

agt ttc agg aaa tgt gaa acc cag ttg tca cag ggc agc taa gaa aag 2976
 Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser Glu Lys
 980 985 990

cca tct tca ttc gtg gag act gtg gcc ctg caa ccc tgg aga agg act 3024
 Pro Ser Ser Phe Val Glu Thr Val Ala Leu Gln Pro Trp Arg Arg Thr
 995 1000 1005

tgc tgg tac tta aaa aat ggg aca ttt gcc acc cag gac tga 3056
 Cys Trp Tyr Leu Lys Asn Gly Thr Phe Ala Thr Gln Asp
 1010 1015 1020

ctgtacactc cctgatcagc cagcactctg gaagctttgg gatcccagga accatggaat 3126

tattcccaaa tggactctga ccagattttt gccatactgg ggggtggcgg gatggaggat 3186

gggtactcag gcactgactgc gtatttatta aagtgtgttt ttccacaatg taccaaaaca 3246

ggcataagca gcttctctctg ctgactggcc aatcactgcc catctgagag atgatttctt 3306

ctggcccata tttgaattta ttggagtaac tcaaattgcc tgaggaaaaa tggaaaaatt 3366

atccaccagt cgattcaaac tgaatttcac tctttatagg aaggcagggc aaactttag 3426

gagtacgaaa cattttcaat aaatctacaa agggaagcct tactacaatt ccaaaaaatca 3486

tcattggttg aaatttgga ggagattatt tgtgaacttg ttaccctttt ggtaattggtg 3546

gactaattgc tgtatagtta tttttgtttt attattactg ttacattaat ttaacatgca 3606

tttatagaag aatacattca aagcactgat gtaggagata caccgtactt ggagcagtca 3666

gccaaaaatc acagatactg ctttctactta aatggaaaca attctccgat aatgctttgc 3726

tttttttctt atgtcactct tgtgtactat ctatttttct cctctctggg accaagtctt 3786

tttttataaa gcaataatat ctctgttttc atttcagaac attgtgctgt ctgtcagcat 3846

atgtatatca gctacaaaat atattcaact ttgacttctt ttgacaaagg acttttaggaa 3906

aaggaggaac aaagacatta tttgagaatt aaattatata tttttaatat gactgtgacc 3966

ttgactgata ataaagatgt aataagaatt gcaagctaaa aaaaaaaaaa aaaaaactcg 4026

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<211> 989

<212> PPT

<213> Homo sapiens

<223> preliminary human CLASP-5

<400> 4

Ser Thr Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys Pro Ser Ile
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Ser Pro Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu
 50 55 60

Gly Glu Gly Ile Ser Glu Val Gln Arg Lys Ala Val Ser Ala Ile His
 65 70 75 80

Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu
 85 90 95

Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile
 100 105 110

Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp Thr Arg
 115 120 125

Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala Gly Ala
 130 135 140

Ile Thr Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe Asn Leu
 145 150 155 160

Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln Tyr Asn
 165 170 175

Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe Leu Trp
 180 185 190

Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile Ala Asp
 195 200 205

Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe Ile Cys
 210 215 220

Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys Val Ser
 225 230 235 240

Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu Glu Glu
 245 250 255

Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg Arg Arg
 260 265 270

Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu Arg Trp
 275 280 285

Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu Asp Lys
 290 295 300

Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn Leu Ala
 305 310 315 320

Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile Ile Gln
 325 330 335

Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe Gly Asp
370 375 380

Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys His Gln
385 390 395 400

Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser Gln Ala
405 410 415

Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala Thr Ser
420 425 430

Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala Ser Leu
435 440 445

Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg Ser Leu
450 455 460

Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln Met Thr
465 470 475 480

Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn Ser Ile
485 490 495

Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro Glu Met
500 505 510

Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala Ser Pro
515 520 525

Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His Thr Lys
530 535 540

Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala Ala Ala
545 550 555 560

Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr Leu Pro
565 570 575

Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu
580 585 590

Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly Val Cys
595 600 605

Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln
610 615 620

Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val Asn Glu
625 630 635 640

Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg
645 650 655

Phe	Phe	Gly	Ser	Lys	Phe	Gly	Asp	Leu	Asp	Glu	Gln	Glu	Phe	Val	Tyr	690	695	700
Lys	Glu	Pro	Ala	Ile	Thr	Lys	Leu	Pro	Glu	Ile	Ser	His	Arg	Leu	Glu	705	710	715
Ala	Phe	Tyr	Gly	Gln	Cys	Phe	Gly	Ala	Glu	Phe	Val	Glu	Val	Ile	Lys	725	730	735
Asp	Ser	Thr	Pro	Val	Asp	Lys	Thr	Lys	Leu	Asp	Pro	Asn	Lys	Ala	Tyr	740	745	750
Ile	Gln	Ile	Thr	Phe	Val	Glu	Pro	Tyr	Phe	Asp	Glu	Tyr	Glu	Met	Lys	755	760	765
Asp	Arg	Val	Thr	Tyr	Phe	Glu	Lys	Asn	Phe	Asn	Leu	Arg	Arg	Phe	Met	770	775	780
Tyr	Thr	Thr	Pro	Phe	Thr	Leu	Glu	Gly	Arg	Pro	Arg	Gly	Glu	Leu	His	785	790	795
Glu	Gln	Tyr	Arg	Arg	Asn	Thr	Val	Leu	Thr	Thr	Met	His	Ala	Phe	Pro	805	810	815
Tyr	Ile	Lys	Thr	Arg	Ile	Ser	Val	Ile	Gln	Lys	Glu	Glu	Phe	Val	Leu	820	825	830
Thr	Pro	Ile	Glu	Val	Ala	Ile	Glu	Asp	Met	Lys	Lys	Lys	Thr	Leu	Gln	835	840	845
Leu	Ala	Val	Ala	Ile	Asn	Gln	Glu	Pro	Pro	Asp	Ala	Lys	Met	Leu	Gln	850	855	860
Met	Val	Leu	Gln	Gly	Ser	Val	Gly	Ala	Thr	Val	Asn	Gln	Gly	Pro	Leu	865	870	875
Glu	Val	Ala	Gln	Val	Phe	Leu	Ala	Glu	Ile	Pro	Ala	Asp	Pro	Lys	Leu	885	890	895
Tyr	Arg	His	His	Asn	Lys	Leu	Arg	Leu	Cys	Phe	Lys	Glu	Phe	Ile	Met	900	905	910
Arg	Cys	Gly	Glu	Ala	Val	Glu	Lys	Asn	Lys	Arg	Leu	Ile	Thr	Ala	Asp	915	920	925
Gln	Arg	Glu	Tyr	Gln	Gln	Glu	Leu	Lys	Lys	Asn	Tyr	Asn	Lys	Leu	Lys	930	935	940
Glu	Asn	Leu	Arg	Pro	Met	Ile	Glu	Arg	Lys	Ile	Pro	Glu	Leu	Tyr	Lys	945	950	955
Pro	Ile	Phe	Arg	Val	Glu	Ser	Gln	Lys	Arg	Asp	Ser	Phe	His	Arg	Ser	965	970	975

<210> 5
<211> 31
<212> PRT
<213> Homo sapiens
<223> preliminary human CLASP-5

<400> 5
Glu Lys Pro Ser Ser Phe Val Glu Thr Val Ala Leu Gln Pro Trp Arg
1 5 10 15
Arg Thr Cys Trp Tyr Leu Lys Asn Gly Thr Phe Ala Thr Gln Asp
20 25 30

<210> 6
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: furin protease
consensus cleavage sequence

<400> 6
Arg Lys Gln Arg
1

<210> 7
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP-5 homolog
of furin protease consensus cleavage sequence

<400> 7
Arg Arg Thr Arg
1

<210> 8
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP-5
immunoreceptor tyrosine-based activation
(ITAM) motif 1

<220>
<221> MOD_RES
<222> 1

<210> 9

<211> 1352

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-2A

<400> 9

Val Leu His His His Gln Asn Pro Glu Phe Tyr Asp Glu Ile Lys Ile
1 5 10 15
Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu Leu Leu Thr Phe
20 25 30
Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser Thr Lys Lys Arg
35 40 45
Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys
50 55 60
Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro val Ser Ala Asn
65 70 75 80
Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His
85 90 95
Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys
100 105 110
Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu
115 120 125
His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala
130 135 140
Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu
145 150 155 160
Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe
165 170 175
Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr
180 185 190
Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu
195 200 205
Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr
210 215 220
Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met
225 230 235 240

Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu	Arg	Asn	Gln	Arg	275	280	285
Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val	Val	Asn	Met	Leu	290	295	300
Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro	Glu	Ala	Ser	Lys	305	310	315
Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	Cys	Phe	Thr	Phe	325	330	335
Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	Tyr	Ile	Ser	Cys	340	345	350
Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr	Lys	Phe	Glu	Phe	355	360	365
Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu	Asn	Leu	Pro	370	375	380
Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln	Asp	Leu	Gln	Leu	385	390	395
Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His	Phe	Leu	Val	Gly	405	410	415
Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu	Phe	Arg	Glu	Val	420	425	430
Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu	Ile	Lys	His	Ser	435	440	445
Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala	Arg	Ile	Ala	Thr	450	455	460
Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn	Val	Gln	Arg	Ile	465	470	475
Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala	Gly	Met	Thr	Val	485	490	495
Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro	Leu	Val	Thr	Pro	500	505	510
Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	Asp	Leu	Leu	Gly	515	520	525
Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser	Thr	Pro	Asn	Ile	530	535	540
Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Ser	Thr	Asp	545	550	555
																560		

Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu	Met	Cys	Phe	Leu
		595					600					605			
Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr	Tyr	Trp	Asn
	610					615					620				
Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	Thr	Ile	Ser	Glu	Val
	625				630					635					640
Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg	Tyr	Ile	Ala	Arg	Asn
				645					650					655	
Gln	Glu	Gly	Leu	Gly	Pro	Ile	Val	His	Asp	Arg	Lys	Ser	Gln	Thr	Leu
			660					665						670	
Pro	Val	Ser	Arg	Asn	Arg	Thr	Gly	Met	Met	His	Ala	Arg	Leu	Gln	Gln
		675					680					685			
Leu	Gly	Ser	Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser	Tyr	Gly	His
	690					695					700				
Ser	Asp	Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala	Asn	Ile	Ala
	705				710					715					720
Thr	Glu	Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu	Phe	Thr	Leu
			725						730					735	
Ala	Phe	Lys	Asn	Gln	Leu	Leu	Ala	Asp	His	Gly	His	Asn	Pro	Leu	Met
			740					745					750		
Lys	Lys	Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys	His	Gln	Ser
		755					760					765			
Glu	Thr	Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser	Leu	Ile	Tyr
	770					775					780				
Lys	Phe	Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	Ala	Ala
	785				790					795					800
Leu	Cys	Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	Ser	Ile
				805					810					815	
Arg	Thr	Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	Asn	Phe
			820					825					830		
Asp	Tyr	Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu	Gln	Val	Ile
		835					840					845			
Ile	Ser	Val	Ser	Gln	Leu	Ile	Ala	Asp	Val	Val	Gly	Ile	Gly	Glu	Thr
	850					855					860				
Arg	Phe	Gln	Gln	Ser	Leu	Ser	Ile	Ile	Asn	Asn	Cys	Ala	Asn	Ser	Asp
	865				870					875					880

Glu	Asn	Asp	Pro	Glu	Met	Leu	Val	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	915	920	925
Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	930	935	940
Ala	Arg	Ile	His	Val	Lys	Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	945	950	955
Tyr	Val	His	Val	Thr	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	Lys	Gly	965	970	975
Val	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val	Ile	Thr	Pro	Asn	Ile	980	985	990
Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly	Met	Gln	Asp	Val	His	995	1000	1005
Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln	Cys	Ala	Asp	Gly	1010	1015	1020
Leu	Trp	Lys	Ala	Glu	Arg	Tyr	Glu	Leu	Ile	Ala	Asp	Ile	Tyr	Lys	Leu	1025	1030	1035
Ile	Ile	Pro	Ile	Tyr	Glu	Lys	Arg	Arg	Asp	Phe	Phe	Glu	Asp	Glu	Asp	1045	1050	1055
Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu	1060	1065	1070
Ile	Ser	Gln	Arg	Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu	1075	1080	1085
Asn	Val	Lys	Met	Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu	1090	1095	1100
Asp	Ser	Lys	Tyr	Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Ile	Pro	Phe	Phe	1105	1110	1115
Asp	Glu	Lys	Glu	Leu	Gln	Glu	Arg	Lys	Thr	Glu	Phe	Glu	Arg	Ser	His	1125	1130	1135
Asn	Ile	Arg	Arg	Phe	Met	Phe	Glu	Met	Pro	Phe	Thr	Gln	Thr	Gly	Lys	1140	1145	1150
Arg	Gln	Gly	Gly	Val	Glu	Glu	Gln	Cys	Lys	Arg	Arg	Thr	Ile	Leu	Thr	1155	1160	1165
Ala	Ile	His	Cys	Phe	Pro	Tyr	Val	Lys	Lys	Arg	Ile	Pro	Val	Met	Tyr	1170	1175	1180
Gln	His	His	Thr	Asp	Leu	Asn	Pro	Ile	Glu	Val	Ala	Ile	Asp	Glu	Met	1185	1190	1195

Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr
 1235 1240 1245
 Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val
 1250 1255 1260
 Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu
 1265 1270 1275 1280
 Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala
 1285 1290 1295
 Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln
 1300 1305 1310
 Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His
 1315 1320 1325
 Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly
 1330 1335 1340
 Met Thr Ser Ser Ser Ser Val Val
 1345 1350

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 <213> Homo sapiens
 <220>
 <223> human KIAA1058

<400> 10
 Ala Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg
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 Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala
 20 25 30
 Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
 35 40 45
 Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
 50 55 60
 Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
 65 70 75 80
 Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
 85 90 95
 His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
 100 105 110

Pro	Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg	145	150	155	160
Ser	Ala	Phe	Ala	Ala	Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr	165	170	175	
Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His	180	185	190	
Leu	Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	195	200	205	
Ser	Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	210	215	220	
Leu	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	225	230	235	240
Pro	Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	Tyr	Leu	Gly	Tyr	Gln	Glu	Leu	245	250	255	
Gly	Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	260	265	270	
Lys	Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	275	280	285	
Gln	Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	290	295	300	
Ser	Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	305	310	315	320
Leu	His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	325	330	335	
Leu	Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	340	345	350	
Ala	Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	355	360	365	
Glu	Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	370	375	380	
Lys	Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	385	390	395	400
Leu	Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	405	410	415	
Thr	Ser	Asn	Lys	Leu	Leu	Lys	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	420	425	430	

Val	Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Arg	Asp	Asn	465	470	475	480
Pro	Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	485	490	495	
Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	500	505	510	
Asn	Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	515	520	525	
Tyr	Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	530	535	540	
Pro	Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	545	550	555	560
Gln	Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	565	570	575	
His	Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	580	585	590	
Glu	Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	595	600	605	
Leu	Ile	Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	610	615	620	
Ala	Arg	Ile	Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	625	630	635	640
Asn	Val	Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	645	650	655	
Ala	Gly	Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	660	665	670	
Pro	Leu	Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	675	680	685	
Lys	Asp	Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	690	695	700	
Ser	Thr	Pro	Asn	Ile	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	705	710	715	720
Leu	Ile	Ser	Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	725	730	735	
Lys	Ser	Asn	Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	740	745	750	

Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe
785 790 795 800

Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg
805 810 815

Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly
820 825 830

Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp
835 840 845

Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu
850 855 860

Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe
865 870 875 880

Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys
885 890 895

Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr
900 905 910

Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe
915 920 925

Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys
930 935 940

Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr
945 950 955 960

Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr
965 970 975

Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser
980 985 990

Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
995 1000 1005

Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
1010 1015 1020

Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
1025 1030 1035 1040

Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
1045 1050 1055

Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
1060 1065 1070

His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
1105 1110 1115 1120

Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg
1125 1130 1135

Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val
1140 1145 1150

Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly
1155 1160 1165

Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu
1170 1175 1180

Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala
1185 1190 1195 1200

Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe
1205 1210 1215

Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
1220 1225 1230

Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
1235 1240 1245

Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
1250 1255 1260

Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
1265 1270 1275 1280

Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
1285 1290 1295

Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
1300 1305 1310

Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
1315 1320 1325

Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
1330 1335 1340

Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg
1345 1350 1355 1360

Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
1365 1370 1375

Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
1380 1385 1390

Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
1425 1430 1435 1440

Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
1445 1450 1455

Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
1460 1465 1470

Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
1475 1480 1485

Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
1490 1495 1500

Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
1505 1510 1515 1520

Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Leu Gly
1525 1530

<210> 11

<211> 738

<212> PRT

<213> Rattus norvegicus

<220>

<223> rat TRG

<400> 11

Lys Leu Ser Arg Gly His Ser Pro Leu Met Lys Lys Val Phe Asp Val
1 5 10 15

Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Met Ala Leu Lys Asn
20 25 30

Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe
35 40 45

Tyr Glu Gly Arg Ala Asp Met Cys Ala Ser Leu Cys Tyr Glu Val Leu
50 55 60

Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln
65 70 75 80

Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys
85 90 95

Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Leu Ser Gln Leu
100 105 110

Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe Gln Gln Ser Leu
115 120 125

Leu Met Ala Thr	Ala Gln Met Lys Glu His Glu Asn Asp	Pro Glu Met
	165 170	175
Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro		
	180 185	190
Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys		
	195 200	205
Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val His Val Thr Ala		
	210 215	220
Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Asp Leu Ala Leu Gln		
	225 230	240
Arg Glu Pro Pro Val Phe Pro Tyr Ser His Thr Ser Cys Gln Arg Lys		
	245 250	255
Ser Arg Gly Gly Met Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile		
	260 265	270
Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met		
	275 280	285
Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln		
	290 295	300
Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Leu Arg Ala Gly Leu Leu		
	305 310	315 320
Thr Ser Ile Asn Ser Ser Ser Pro Ser Met Lys Ser Gly Gly Thr Leu		
	325 330	335
Glu Thr Thr His Leu Tyr Asp Thr Leu His Arg Pro Tyr Ser Lys Val		
	340 345	350
Thr Glu Val Ile Thr Arg Ala Ala Gly Ser Trp Asp Leu Leu Pro Gly		
	355 360	365
Gly Leu Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr		
	370 375	380
Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg		
	385 390	395 400
Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met		
	405 410	415
Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe		
	420 425	430
Ala Tyr Ile Gln Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu		
	435 440	445

Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
 485 490 495
 Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
 500 505 510
 Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
 515 520 525
 Ala Glu Leu His Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 530 535 540
 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 545 550 555 560
 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 565 570 575
 Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
 580 585 590
 Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
 595 600 605
 Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
 610 615 620
 Ile Arg Lys Glu Leu Ser Asp Ile Ile Val Pro Arg Ile Cys Pro Gly
 625 630 635 640
 Glu Asp Lys Arg Ala Thr Lys Phe Pro Ala His Leu Gln Arg His Gln
 645 650 655
 Arg Asp Thr Asn Lys His Ser Gly Ser Arg Val Asp Gln Phe Ile Leu
 660 665 670
 Ser Cys Val Thr Leu Pro His Glu Pro His Val Gly Thr Cys Phe Val
 675 680 685
 Met Cys Lys Leu Arg Thr Thr Phe Arg Ala Asn His Trp Phe Cys Gln
 690 695 700
 Ala Gln Glu Glu Ala Met Gly Asn Gly Arg Glu Lys Glu Pro Trp Thr
 705 710 715 720
 Val Ile Phe Asn Ser Arg Phe Tyr Arg Ser Trp Gly Lys Val His Ile
 725 730 735

Phe Phe

<210> 12

<211> 1214

<212> PRT

<400> 12

Met Glu Ile Gln Val Leu Ile Arg Phe Leu Ser Val Ile Leu Met Gln
1 5 10 15

Leu Phe Trp Val Leu Pro Asn Met Ile His Glu Asp Asp Val Pro Ile
20 25 30

Ser Cys Pro Met Val Leu Phe His Ile Val Ser Lys Cys His Glu Glu
35 40 45

Gly Leu Asp Ser Tyr Leu Ser Ser Phe Ile Lys Tyr Ser Phe Arg Pro
50 55 60

Gly Lys Pro Ser Ala Pro Gln Ala Pro Leu Ile His Glu Thr Leu Ala
65 70 75 80

Thr Met Met Ile Ala Leu Leu Lys Gln Ser Ala Asp Phe Leu Ala Ile
85 90 95

Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Glu Ile Ile Ala Lys
100 105 110

Ser Met Ala Thr Tyr Leu Leu Glu Glu Asn Lys Ile Lys Leu Thr His
115 120 125

Gly Gln Arg Phe Pro Lys Ala Tyr His His Ala Leu His Ser Leu Phe
130 135 140

Leu Ala Ile Thr Ile Val Glu Ser Gln Tyr Ala Glu Ile Pro Lys Glu
145 150 155 160

Ser Arg Asn Val Asn Tyr Ser Leu Ala Ser Phe Leu Lys Cys Cys Leu
165 170 175

Thr Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Asn Asp Tyr Ile
180 185 190

Ser Gly Phe Ser Pro Lys Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe
195 200 205

Glu Phe Leu Gln Thr Ile Cys Asn His Glu His Tyr Ile Pro Leu Asn
210 215 220

Leu Pro Met Ala Phe Ala Lys Pro Lys Leu Gln Arg Val Gln Asp Ser
225 230 235 240

Asn Leu Glu Tyr Ser Leu Ser Asp Glu Tyr Cys Lys His His Phe Leu
245 250 255

Val Gly Leu Leu Leu Arg Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr
260 265 270

Glu Ile Arg Tyr Thr Ala Ile Ser Val Ile Lys Asn Leu Leu Ile Lys
275 280 285

Arg Leu Ala Gly Arg Asp Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn
 325 330 335
 Ser Ala Ser Arg Asp Glu Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn
 340 345 350
 Arg Gly Ser Leu Ser Thr Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln
 355 360 365
 Asn Gly His Gly Ile Lys Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro
 370 375 380
 Glu Gly Ala Thr Gly Phe Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr
 385 390 395 400
 Arg Gln Ser Ser Thr Arg Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp
 405 410 415
 Gln Tyr Glu Ile Arg Ser Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys
 420 425 430
 Met Ile Ser Glu Asp Thr Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro
 435 440 445
 Gln Glu Leu Ile Asn Ile Leu Ile Leu Leu Glu Val Cys Leu Phe His
 450 455 460
 Phe Arg Tyr Met Gly Lys Arg Asn Ile Ala Arg Val His Asp Ala Trp
 465 470 475 480
 Leu Ser Lys His Phe Gly Ile Asp Arg Lys Ser Gln Thr Met Pro Ala
 485 490 495
 Leu Arg Asn Arg Ser Gly Val Met Gln Ala Arg Leu Gln His Leu Ser
 500 505 510
 Ser Leu Glu Ser Ser Phe Thr Leu Asn His Ser Ser Thr Thr Thr Glu
 515 520 525
 Ala Asp Ile Phe His Gln Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu
 530 535 540
 Val Ser Leu Thr Val Leu Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe
 545 550 555 560
 Lys Thr His Phe Leu Asn Asn Asp Gly His Asn Pro Leu Met Lys Lys
 565 570 575
 Val Phe Asp Ile His Leu Ala Phe Leu Lys Asn Gly Gln Ser Glu Val
 580 585 590
 Ser Leu Lys His Val Phe Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe
 595 600 605

Glu	Ala	Ser	Ala	Leu	Leu	Tyr	Leu	Leu	Met	Arg	Asn	Asn	Phe	Glu	Tyr	645	650	655	
Thr	Lys	Arg	Lys	Thr	Phe	Leu	Arg	Thr	His	Leu	Gln	Ile	Ile	Ile	Ala	660	665	670	
Val	Ser	Gln	Leu	Ile	Ala	Asp	Val	Ala	Leu	Ser	Gly	Gly	Ser	Arg	Phe	675	680	685	
Gln	Glu	Ser	Leu	Phe	Ile	Ile	Asn	Asn	Phe	Ala	Asn	Ser	Asp	Arg	Pro	690	695	700	
Met	Leu	Ala	Arg	Ala	Phe	Pro	Ala	Glu	Val	Lys	Asp	Leu	Thr	Lys	Arg	705	710	715	720
Ile	Arg	Thr	Val	Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	725	730	735	
Asp	Pro	Glu	Met	Leu	Ile	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	Ser	Tyr	740	745	750	
Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	Ala	Lys	755	760	765	
Ile	His	Val	Lys	Asn	Gly	Asp	Phe	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Val	770	775	780	
His	Val	Ala	Ala	Leu	Val	Ala	Glu	Phe	Leu	His	Arg	Lys	Lys	Leu	Phe	785	790	795	800
Pro	Asn	Gly	Cys	Ser	Ala	Phe	Lys	Lys	Ile	Thr	Pro	Asn	Ile	Asp	Glu	805	810	815	
Glu	Gly	Ala	Met	Lys	Glu	Asp	Ala	Gly	Met	Met	Asp	Val	His	Tyr	Ser	820	825	830	
Glu	Glu	Val	Leu	Leu	Glu	Leu	Leu	Glu	Gln	Cys	Val	Asn	Gly	Leu	Trp	835	840	845	
Lys	Ala	Glu	Arg	Tyr	Glu	Ile	Ile	Ser	Glu	Ile	Ser	Lys	Leu	Ile	Gly	850	855	860	
Pro	Ile	Tyr	Glu	Asn	Arg	Arg	Glu	Phe	Glu	Asn	Leu	Thr	Gln	Val	Tyr	865	870	875	880
Arg	Thr	Leu	His	Gly	Ala	Tyr	Thr	Lys	Ile	Leu	Glu	Val	Met	His	Thr	885	890	895	
Lys	Lys	Arg	Leu	Leu	Gly	Thr	Phe	Phe	Arg	Val	Ala	Phe	Tyr	Gly	Gln	900	905	910	
Ser	Phe	Phe	Glu	Glu	Glu	Asp	Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	915	920	925	

Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln Val
965 970 975

Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys
980 985 990

Thr Glu Phe Glu Arg Asn His Asn Ile Ser Arg Phe Val Phe Glu Ala
995 1000 1005

Pro Tyr Thr Leu Ser Gly Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys
1010 1015 1020

Lys Arg Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys
1025 1030 1035 1040

Lys Arg Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile
1045 1050 1055

Asp Gly Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys
1060 1065 1070

Leu Cys Ser Ser Thr Asp Val Asp Met Ile Gln Leu Gln Leu Lys Leu
1075 1080 1085

Gln Gly Trp Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala
1090 1095 1100

Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys
1105 1110 1115 1120

Val Ser Glu Leu Lys Asp Met Phe Arg Lys Phe Ile Gln Ala Cys Ser
1125 1130 1135

Ile Ala Leu Glu Leu Asn Glu Arg Leu Ile Lys Glu Asp Gln Val Glu
1140 1145 1150

Tyr His Glu Gly Leu Lys Ser Asn Phe Arg Asp Met Val Lys Glu Leu
1155 1160 1165

Ser Asp Ile Ile His Glu Gln Ile Leu Gln Glu Asp Thr Met His Ser
1170 1175 1180

Pro Trp Met Ser Asn Thr Leu His Val Phe Cys Ala Ile Ser Gly Thr
1185 1190 1195 1200

Ser Ser Asp Arg Gly Tyr Gly Ser Pro Arg Tyr Ala Glu Val
1205 1210

<210> 13

<211> 1288

<212> PRT

<213> Homo sapiens

Gln Asn Glu Glu Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro
 20 25 30
 Asp Ile Val Ala Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln
 35 40 45
 Ser Tyr Ile Lys Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro
 50 55 60
 Val His Glu Asp Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn
 65 70 75 80
 Asp Ser Pro Thr Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe
 85 90 95
 Ala Ile Ile Leu Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys
 100 105 110
 Ile Gln Leu Pro Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu
 115 120 125
 Leu Asp Asn Leu Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr
 130 135 140
 Lys Asp Ala Leu Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg
 145 150 155 160
 Phe Leu Lys Arg Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys
 165 170 175
 Met Val Asn Asn Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr
 180 185 190
 Leu Cys Gln Tyr Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu
 195 200 205
 His Phe Ile Pro Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp
 210 215 220
 Pro Leu Thr Pro Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met
 225 230 235 240
 Pro Glu Tyr Ser Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile
 245 250 255
 Gly Ile Leu Leu Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp
 260 265 270
 Val Arg His Leu Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His
 275 280 285
 Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala
 290 295 300
 Gln Ile Thr Met Thr Glu Thr Glu Met Tyr Ile Leu Thr Met Thr Ile

Gly	Ser	Arg	Asp	Asp	Leu	Ser	Thr	Asn	Gly	Gly	Phe	Gln	Ser	Gln	Thr		
			340					345					350				
Ala	Ile	Lys	His	Ala	Asn	Ser	Val	Asp	Thr	Ser	Phe	Ser	Lys	Asp	Val		
		355					360					365					
Leu	Asn	Ser	Ile	Ala	Ala	Phe	Ser	Ser	Ile	Ala	Ile	Ser	Thr	Val	Asn		
	370					375					380						
His	Ala	Asp	Ser	Arg	Ala	Ser	Leu	Ala	Ser	Leu	Asp	Ser	Asn	Pro	Ser		
385					390					395					400		
Thr	Asn	Glu	Lys	Ser	Ser	Glu	Lys	Thr	Asp	Asn	Cys	Glu	Lys	Ile	Pro		
			405						410					415			
Arg	Pro	Leu	Ala	Leu	Ile	Gly	Ser	Thr	Leu	Arg	Phe	Asp	Arg	Leu	Asp		
		420						425					430				
Gln	Ala	Glu	Thr	Arg	Ser	Leu	Leu	Met	Cys	Phe	Leu	His	Ile	Met	Lys		
	435						440					445					
Thr	Ile	Ser	Tyr	Glu	Thr	Leu	Ile	Ala	Tyr	Trp	Gln	Arg	Ala	Pro	Ser		
	450					455					460						
Pro	Glu	Val	Ser	Asp	Phe	Phe	Ser	Ile	Leu	Asp	Val	Cys	Leu	Gln	Asn		
465					470					475					480		
Phe	Arg	Tyr	Leu	Gly	Lys	Arg	Asn	Ile	Ile	Arg	Lys	Ile	Ala	Ala	Ala		
			485						490					495			
Phe	Lys	Phe	Val	Gln	Ser	Thr	Gln	Asn	Asn	Gly	Thr	Leu	Lys	Gly	Ser		
		500						505					510				
Asn	Pro	Ser	Cys	Gln	Thr	Ser	Gly	Leu	Leu	Ala	Gln	Trp	Met	His	Ser		
	515						520					525					
Thr	Ser	Arg	His	Glu	Gly	His	Lys	Gln	His	Arg	Ser	Gln	Thr	Leu	Pro		
	530					535					540						
Ile	Ile	Arg	Gly	Lys	Asn	Ala	Leu	Ser	Asn	Pro	Lys	Leu	Leu	Gln	Met		
545					550					555					560		
Leu	Asp	Asn	Thr	Met	Thr	Ser	Asn	Ser	Asn	Glu	Ile	Asp	Ile	Val	His		
			565						570					575			
His	Val	Asp	Thr	Glu	Ala	Asn	Ile	Ala	Thr	Glu	Gly	Cys	Leu	Thr	Ile		
		580					585						590				
Leu	Asp	Leu	Val	Ser	Leu	Phe	Thr	Gln	Thr	His	Gln	Arg	Gln	Leu	Gln		
	595						600					605					
Gln	Cys	Asp	Cys	Gln	Asn	Ser	Leu	Met	Lys	Arg	Gly	Phe	Asp	Thr	Tyr		
	610					615					620						

Gln	Gly	Pro	Ala	Asp	Leu	Cys	Gly	Ser	Phe	Cys	Tyr	Glu	Val	Leu	Lys	660	665	670
Cys	Cys	Asn	His	Arg	Ser	Arg	Ser	Thr	Gln	Thr	Glu	Ala	Ser	Ala	Leu	675	680	685
Leu	Tyr	Leu	Phe	Met	Arg	Lys	Asn	Phe	Glu	Phe	Asn	Lys	Gln	Lys	Ser	690	695	700
Ile	Val	Arg	Ser	His	Leu	Gln	Leu	Ile	Lys	Ala	Val	Ser	Gln	Leu	Ile	705	710	715
Ala	Asp	Ala	Gly	Ile	Gly	Gly	Ser	Arg	Phe	Gln	His	Ser	Leu	Ala	Ile	725	730	735
Thr	Asn	Asn	Phe	Ala	Asn	Gly	Asp	Lys	Gln	Met	Lys	Asn	Ser	Asn	Phe	740	745	750
Pro	Ala	Glu	Val	Lys	Asp	Leu	Thr	Lys	Arg	Ile	Arg	Thr	Val	Leu	Met	755	760	765
Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	Asp	Pro	Glu	Met	Leu	Val	770	775	780
Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Asn	Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	785	790	795
Arg	Arg	Thr	Trp	Leu	Glu	Ser	Met	Ala	Lys	Ile	His	Ala	Arg	Asn	Gly	805	810	815
Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Ile	His	Ile	Ala	Ala	Leu	Ile	820	825	830
Ala	Glu	Tyr	Leu	Lys	Arg	Lys	Gly	Tyr	Trp	Lys	Val	Glu	Lys	Ile	Cys	835	840	845
Thr	Ala	Ser	Leu	Leu	Ser	Glu	Asp	Thr	His	Pro	Cys	Asp	Ser	Asn	Ser	850	855	860
Leu	Leu	Thr	Thr	Pro	Ser	Gly	Gly	Ser	Met	Phe	Ser	Met	Gly	Trp	Pro	865	870	875
Ala	Phe	Leu	Ser	Ile	Thr	Pro	Asn	Ile	Lys	Glu	Glu	Gly	Ala	Ala	Lys	885	890	895
Glu	Asp	Ser	Gly	Met	His	Asp	Thr	Pro	Tyr	Asn	Glu	Asn	Ile	Leu	Val	900	905	910
Glu	Gln	Leu	Tyr	Met	Cys	Gly	Glu	Phe	Leu	Trp	Lys	Ser	Glu	Arg	Tyr	915	920	925
Glu	Leu	Ile	Ala	Asp	Val	Asn	Lys	Pro	Ile	Ile	Ala	Val	Phe	Glu	Lys	930	935	940

Gly Arg Tyr Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu
980 985 990

Glu Glu Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu
995 1000 1005

Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly
1010 1015 1020

Ala Asp Asn Val Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys
1025 1030 1035 1040

Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro
1045 1050 1055

Phe Phe Glu Glu Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met
1060 1065 1070

His His Asn Ile Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser
1075 1080 1085

Gly Lys Lys His Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile
1090 1095 1100

Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val
1105 1110 1115 1120

Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp
1125 1130 1135

Glu Met Ser Arg Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu
1140 1145 1150

Glu Val Asp Met Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser
1155 1160 1165

Val Lys Val Asn Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu
1170 1175 1180

Glu Thr Asn Ala Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys
1185 1190 1195 1200

Glu Ile Phe Arg Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val
1205 1210 1215

Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu
1220 1225 1230

Arg Ser His Tyr Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn
1235 1240 1245

Glu Gln Ile Thr Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln
1250 1255 1260

<210> 14
<211> 1220
<212> PRT
<213> Homo sapiens

<220>
<223> human CLASP-3

<400> 14

Gly	Pro	Gly	Pro	Ala	Arg	Ser	Thr	Val	Ser	Ile	Ser	Leu	Ile	Ser	Asn	
1				5					10					15		
Ser	Ala	Arg	Val	Asn	Arg	Ser	Arg	Ser	Leu	Ser	Asn	Ser	Asn	Pro	Asp	
			20					25					30			
Ile	Ser	Gly	Thr	Pro	Thr	Ser	Pro	Asp	Asp	Glu	Val	Arg	Ser	Ile	Ile	
		35					40					45				
Gly	Ser	Lys	Gly	Leu	Asp	Arg	Ser	Asn	Ser	Trp	Val	Asn	Thr	Gly	Gly	
	50					55					60					
Pro	Lys	Ala	Ala	Pro	Trp	Gly	Ser	Asn	Pro	Ser	Pro	Ser	Ala	Glu	Ser	
	65				70					75				80		
Thr	Gln	Ala	Met	Asp	Arg	Ser	Cys	Asn	Arg	Met	Ser	Ser	His	Thr	Glu	
				85					90					95		
Thr	Ser	Ser	Phe	Leu	Gln	Thr	Leu	Thr	Gly	Arg	Leu	Pro	Thr	Lys	Lys	
			100					105					110			
Leu	Phe	His	Glu	Glu	Leu	Ala	Leu	Gln	Trp	Val	Val	Cys	Ser	Gly	Ser	
		115					120					125				
Val	Arg	Glu	Ser	Ala	Leu	Gln	Gln	Ala	Trp	Phe	Phe	Phe	Glu	Leu	Met	
	130					135					140					
Val	Lys	Ser	Met	Val	His	His	Leu	Tyr	Phe	Asn	Asp	Lys	Leu	Glu	Ala	
	145				150					155				160		
Pro	Arg	Lys	Ser	Arg	Phe	Pro	Glu	Arg	Phe	Met	Asp	Asp	Ile	Ala	Ala	
				165					170					175		
Leu	Val	Ser	Thr	Ile	Ala	Ser	Asp	Ile	Val	Ser	Arg	Phe	Gln	Lys	Asp	
			180					185					190			
Thr	Glu	Met	Val	Glu	Arg	Leu	Asn	Thr	Ser	Leu	Ala	Phe	Phe	Leu	Asn	
		195					200					205				
Asp	Leu	Leu	Ser	Val	Met	Asp	Arg	Gly	Phe	Val	Phe	Ser	Leu	Ile	Lys	
	210					215					220					
Ser	Cys	Tyr	Lys	Gln	Val	Ser	Ser	Lys	Leu	Tyr	Ser	Leu	Pro	Asn	Pro	
	225				230					235				240		

Pro Ala Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser
 275 280 285
 Gly Phe Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu
 290 295 300
 Leu Ser Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu
 305 310 315 320
 Thr Glu Leu Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly
 325 330 335
 Leu His Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His
 340 345 350
 Asp Ser Asp Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val Ala
 355 360 365
 Met Leu Tyr Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro Gln
 370 375 380
 Leu Tyr Asp Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile Cys
 385 390 395 400
 Ile Ala Thr Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser Gln
 405 410 415
 Thr Val Ala Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr Arg
 420 425 430
 Pro Gly Ser Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr Thr
 435 440 445
 Phe Ser Ala Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp Val
 450 455 460
 Leu Lys Asn Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp Leu
 465 470 475 480
 Ser Val Leu Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys Val
 485 490 495
 Ser Cys Phe Glu Tyr Lys Gly Lys Lys Val Phe Glu Arg Met Asn Ser
 500 505 510
 Leu Thr Phe Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu Ala
 515 520 525
 Ile Leu Gly Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg
 530 535 540
 Gly Gln Leu Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln Glu
 545 550 555 560

Gly	Asn	Leu	Ala	Thr	Glu	Ala	Asn	Leu	Ile	Ile	Leu	Asp	Thr	Leu	Glu	595	600	605
Ile	Val	Val	Gln	Thr	Val	Ser	Val	Thr	Glu	Ser	Lys	Glu	Ser	Ile	Leu	610	615	620
Gly	Gly	Val	Leu	Lys	Val	Leu	Leu	His	Ser	Met	Ala	Cys	Asn	Gln	Ser	625	630	635
Ala	Val	Tyr	Leu	Gln	His	Cys	Phe	Ala	Thr	Gln	Arg	Ala	Leu	Val	Ser	645	650	655
Lys	Phe	Pro	Glu	Leu	Leu	Phe	Glu	Glu	Glu	Thr	Glu	Gln	Cys	Ala	Asp	660	665	670
Leu	Cys	Leu	Arg	Leu	Leu	Arg	His	Cys	Ser	Ser	Ser	Ile	Gly	Thr	Ile	675	680	685
Arg	Ser	His	Pro	Ser	Ala	Ser	Leu	Tyr	Leu	Leu	Met	Arg	Gln	Asn	Phe	690	695	700
Glu	Ile	Gly	Asn	Asn	Phe	Ala	Arg	Val	Lys	Met	Gln	Val	Pro	Met	Ser	705	710	715
Leu	Ser	Ser	Leu	Val	Gly	Thr	Ser	Gln	Asn	Phe	Asn	Glu	Glu	Phe	Leu	725	730	735
Arg	Arg	Ser	Leu	Lys	Thr	Ile	Leu	Thr	Tyr	Ala	Glu	Glu	Asp	Leu	Glu	740	745	750
Leu	Arg	Glu	Thr	Thr	Phe	Pro	Asp	Gln	Val	Gln	Asp	Leu	Val	Phe	Asn	755	760	765
Leu	His	Met	Ile	Leu	Ser	Asp	Thr	Val	Lys	Met	Lys	Glu	His	Gln	Glu	770	775	780
Asp	Pro	Glu	Met	Leu	Ile	Asp	Leu	Met	Tyr	Arg	Ile	Ala	Lys	Gly	Tyr	785	790	795
Gln	Thr	Ser	Pro	Asp	Leu	Arg	Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Gly	805	810	815
Lys	His	Ser	Glu	Arg	Ser	Asn	His	Ala	Glu	Ala	Ala	Gln	Cys	Leu	Val	820	825	830
His	Ser	Ala	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Ser	Met	Leu	Glu	Asp	Arg	835	840	845
Lys	Tyr	Leu	Pro	Val	Gly	Cys	Val	Thr	Phe	Gln	Asn	Ile	Ser	Ser	Asn	850	855	860
Val	Leu	Glu	Glu	Ser	Ala	Val	Ser	Asp	Asp	Val	Val	Ser	Pro	Asp	Glu	865	870	875

Ala Val Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn
 915 920 925
 Arg Asp Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala
 930 935 940
 Phe Ser Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly
 945 950 955 960
 Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp
 965 970 975
 Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu
 980 985 990
 Ile Ser His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp
 995 1000 1005
 Val Val Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu
 1010 1015 1020
 Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe
 1025 1030 1035 1040
 Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr
 1045 1050 1055
 Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg
 1060 1065 1070
 Ala His Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr
 1075 1080 1085
 Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His
 1090 1095 1100
 Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met
 1105 1110 1115 1120
 Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala
 1125 1130 1135
 Asp Pro Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr
 1140 1145 1150
 Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile
 1155 1160 1165
 Pro Ser Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys
 1170 1175 1180
 Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys
 1185 1190 1195 1200

<210> 15

<211> 987

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-5

<400> 15

Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys Pro Ser Ile Ser Ser
1 5 10 15

Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp Gln Lys Ile Ala Ser
20 25 30

Met Phe Asp Arg Thr Ser Arg Val Pro Ala Ser Ser Thr Ser Ser Pro
35 40 45

Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu Gly Glu
50 55 60

Gly Ile Ser Glu Val Gln Arg Lys Ala Val Ser Ala Ile His Ser Leu
65 70 75 80

Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu Val Lys
85 90 95

Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile Leu Asp
100 105 110

Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp Thr Arg Arg Tyr
115 120 125

Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala Gly Ala Ile Thr
130 135 140

Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe Asn Leu Lys Thr
145 150 155 160

Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln Tyr Asn Met Leu
165 170 175

Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe Leu Trp Ile Met
180 185 190

Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile Ala Asp Leu Pro
195 200 205

Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe Ile Cys Val Leu
210 215 220

Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys Val Ser Thr Gln
225 230 235 240

Gly	Asn	Asp	Arg	Phe	Pro	Gly	Leu	Asn	Glu	Asn	Leu	Arg	Trp	Lys	Lys	275	280	285
Glu	Gln	Thr	His	Trp	Arg	Gln	Ala	Asn	Glu	Lys	Leu	Asp	Lys	Thr	Lys	290	295	300
Ala	Glu	Leu	Asp	Gln	Glu	Ala	Leu	Ile	Ser	Gly	Asn	Leu	Ala	Thr	Glu	305	310	315
Ala	His	Leu	Ile	Ile	Leu	Asp	Met	Gln	Glu	Asn	Ile	Ile	Gln	Ala	Ser	325	330	335
Ser	Ala	Leu	Asp	Cys	Lys	Asp	Ser	Leu	Leu	Gly	Gly	Val	Leu	Arg	Val	340	345	350
Leu	Val	Asn	Ser	Leu	Asn	Cys	Asp	Gln	Ser	Thr	Thr	Tyr	Leu	Thr	His	355	360	365
Cys	Phe	Ala	Thr	Leu	Arg	Ala	Leu	Ile	Ala	Lys	Phe	Gly	Asp	Leu	Leu	370	375	380
Phe	Glu	Glu	Glu	Val	Glu	Gln	Cys	Phe	Asp	Leu	Cys	His	Gln	Val	Leu	385	390	395
His	His	Cys	Ser	Ser	Ser	Met	Asp	Val	Thr	Arg	Ser	Gln	Ala	Cys	Ala	405	410	415
Thr	Leu	Tyr	Leu	Leu	Met	Arg	Phe	Ser	Phe	Gly	Ala	Thr	Ser	Asn	Phe	420	425	430
Ala	Arg	Val	Lys	Met	Gln	Val	Thr	Met	Ser	Leu	Ala	Ser	Leu	Val	Gly	435	440	445
Arg	Ala	Pro	Asp	Phe	Asn	Glu	Glu	His	Leu	Arg	Arg	Ser	Leu	Arg	Thr	450	455	460
Ile	Leu	Ala	Tyr	Ser	Glu	Glu	Asp	Thr	Ala	Met	Gln	Met	Thr	Pro	Phe	465	470	475
Pro	Thr	Gln	Val	Glu	Glu	Leu	Leu	Cys	Asn	Leu	Asn	Ser	Ile	Leu	Tyr	485	490	495
Asp	Thr	Val	Lys	Met	Arg	Glu	Phe	Gln	Glu	Asp	Pro	Glu	Met	Leu	Met	500	505	510
Asp	Leu	Met	Tyr	Arg	Ile	Ala	Lys	Ser	Tyr	Gln	Ala	Ser	Pro	Asp	Leu	515	520	525
Arg	Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Glu	Lys	His	Thr	Lys	Lys	Lys	530	535	540
Cys	Tyr	Thr	Glu	Ala	Ala	Met	Cys	Leu	Val	His	Ala	Ala	Ala	Leu	Val	545	550	555

Val	Ser	Glu	Asp	Thr	Leu	Ser	Pro	Asp	Glu	Asp	Gly	Val	Cys	Ala	Gly	595	600	605
Gln	Tyr	Phe	Thr	Glu	Ser	Gly	Leu	Val	Gly	Leu	Leu	Glu	Gln	Ala	Ala	610	615	620
Glu	Leu	Phe	Ser	Thr	Gly	Gly	Leu	Tyr	Glu	Thr	Val	Asn	Glu	Val	Tyr	625	630	635
Lys	Leu	Val	Ile	Pro	Ile	Leu	Glu	Ala	His	Arg	Glu	Phe	Arg	Lys	Leu	645	650	655
Thr	Leu	Thr	His	Ser	Lys	Leu	Gln	Arg	Ala	Phe	Asp	Ser	Ile	Val	Asn	660	665	670
Lys	Asp	His	Lys	Arg	Met	Phe	Gly	Thr	Tyr	Phe	Arg	Val	Gly	Phe	Phe	675	680	685
Gly	Ser	Lys	Phe	Gly	Asp	Leu	Asp	Glu	Gln	Glu	Phe	Val	Tyr	Lys	Glu	690	695	700
Pro	Ala	Ile	Thr	Lys	Leu	Pro	Glu	Ile	Ser	His	Arg	Leu	Glu	Ala	Phe	705	710	715
Tyr	Gly	Gln	Cys	Phe	Gly	Ala	Glu	Phe	Val	Glu	Val	Ile	Lys	Asp	Ser	725	730	735
Thr	Pro	Val	Asp	Lys	Thr	Lys	Leu	Asp	Pro	Asn	Lys	Ala	Tyr	Ile	Gln	740	745	750
Ile	Thr	Phe	Val	Glu	Pro	Tyr	Phe	Asp	Glu	Tyr	Glu	Met	Lys	Asp	Arg	755	760	765
Val	Thr	Tyr	Phe	Glu	Lys	Asn	Phe	Asn	Leu	Arg	Arg	Phe	Met	Tyr	Thr	770	775	780
Thr	Pro	Phe	Thr	Leu	Glu	Gly	Arg	Pro	Arg	Gly	Glu	Leu	His	Glu	Gln	785	790	795
Tyr	Arg	Arg	Asn	Thr	Val	Leu	Thr	Thr	Met	His	Ala	Phe	Pro	Tyr	Ile	805	810	815
Lys	Thr	Arg	Ile	Ser	Val	Ile	Gln	Lys	Glu	Glu	Phe	Val	Leu	Thr	Pro	820	825	830
Ile	Glu	Val	Ala	Ile	Glu	Asp	Met	Lys	Lys	Lys	Thr	Leu	Gln	Leu	Ala	835	840	845
Val	Ala	Ile	Asn	Gln	Glu	Pro	Pro	Asp	Ala	Lys	Met	Leu	Gln	Met	Val	850	855	860
Leu	Gln	Gly	Ser	Val	Gly	Ala	Thr	Val	Asn	Gln	Gly	Pro	Leu	Glu	Val	865	870	875
																		880

Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr Ala Asp Gln Arg
915 920 925

Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys Glu Asn
930 935 940

Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys Pro Ile
945 950 955 960

Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His Arg Ser Ser Phe
965 970 975

Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
980 985

<210> 16

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-1

<400> 16

Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 17

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human KIAA1058

<400> 17

Phe Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp
1 5 10 15

Ser Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu
20 25 30

Tyr Ile Tyr Lys Glu Pro
35

<210> 18

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-2

<400> 18

Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
1 5 10

<210> 19

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-6

<400> 19

Phe Arg Val Ala Phe Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 20

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-4

<400> 20

Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu Asp Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 21

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK180

<400> 21

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Thr Phe Leu Arg Gly
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 22

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK2

<400> 22

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 23

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK3

<400> 23

Phe Arg Val Gly Phe Tyr Gly Arg Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15

Lys Glu Tyr Val Cys Arg Gly His
20

<210> 24

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human KIAA0716

<400> 24

Phe Arg Val Gly Phe Tyr Gly Lys Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15

Lys Glu Phe Val Cys Arg Gly His
20

<210> 25

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP 3

Glu Phe Val Tyr Lys Glu Ile

20

<210> 26
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motif C
from rat TRG

<400> 26
Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15
Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser
20 25 30
Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe Ala Tyr Ile Gln
35 40 45
Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
50 55 60

<210> 27
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-1

<400> 27
Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15
Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln Asp Ser
20 25 30
Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln
35 40 45
Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu
50 55 60

<210> 28
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-2

Pro Ser Asp Lys Phe Gly Ser His Asn Val Lys Met Thr Gln Asp Ser
20 25 30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
 35 40 45

Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
 50 55 60

<210> 29
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from human CLASP-4

<400> 29
 Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu
 1 5 10 15

Tyr Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser
 20 25 30

Asp Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln
 35 40 45

Val Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu
 50 55 60

<210> 30
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from human CLASP-3

<400> 30
 Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe
 1 5 10 15

Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser
 20 25 30

Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
 35 40 45

Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu
 50 55 60

<210> 31

<223> Description of Artificial Sequence:DOCK motif C
 from human KIAA0316

<400> 31

His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Asn Glu
1 5 10 15

Phe Pro His Ala Ile Ala Met Gln His Ala Asn Gln Pro Asp Glu Thr
20 25 30

Ile Phe Gln Ala Glu Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
35 40 45

Ile Pro Glu Ser Gln Glu
50

<210> 32

<211> 54

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from canonical DOCK3

<400> 32

His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Ser Glu
1 5 10 15

Phe Pro Gln Ala Val Ala Met Gln His Pro Asn His Pro Asp Asp Ala
20 25 30

Ile Leu Gln Cys Asp Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
35 40 45

Ile Pro Asp Tyr Val Asp
50

<210> 33

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from Canonical DOCK2

<400> 33

Phe Gln Met Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn
1 5 10 15

Thr Thr Ser Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr
20 25 30

Ile Gln Cys Phe Thr Val Gln Pro Val Leu Asn Glu His Pro

<210> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from Canonical DOCK180

<400> 34

Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln Leu Met Thr Gln Phe
1 5 10 15

Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala Pro Gly Asp Asp Val
20 25 30

Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe Thr Val Gln Pro Val
35 40 45

Leu Asp Glu His Pro
50

<210> 35

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-1

<400> 35

Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val
20 25 30

Ala Ile Asp Glu Met Ser Arg Lys Val Ser Glu Leu Asn
35 40 45

<210> 36

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from rat TPG

<400> 36

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30

<210> 37
<211> 45
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human KIAA1058

<400> 37
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15
Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30
Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40 45

<210> 38
<211> 45
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-2

<400> 38
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15
Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30
Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40 45

<210> 39
<211> 44
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-6

<400> 39
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15
Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val

<210> 40
<211> 45
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-4

<400> 40

Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Val
20 25 30

Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln
35 40 45

<210> 41
<211> 45
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-3

<400> 41

Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg
1 5 10 15

Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val
20 25 30

Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala
35 40 45

<210> 42
<211> 45
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-5

<400> 42

Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile Lys Thr Arg
1 5 10 15

Ile Ser Val Ile Glu Lys Glu Glu Phe Val Leu Thr Pro Ile Glu Val

<210> 43

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human KIAA0716

<400> 43

Arg Thr Ser Leu Tyr Leu Val Gln Ser Leu Pro Gly Ile Ser Arg Trp
1 5 10 15

Phe Glu Val Glu Lys Arg Glu Val Val Glu Met Ser Pro Leu Glu Asn
20 25 30

Ala Ile Glu Val Leu Glu Asn Lys Asn Gln Gln Leu Lys
35 40 45

<210> 44

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from canonical DOCK2

<400> 44

Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
1 5 10 15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
20 25 30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
35 40 45

<210> 45

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from canonical DOCK3

<400> 45

Arg Thr Thr Leu Thr Leu Thr His Ser Leu Pro Gly Ile Ser Arg Trp
1 5 10 15

Phe Glu Val Glu Arg Arg Glu Leu Val Glu Val Ser Pro Leu Glu Asn

<210> 46
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
and E from canonical DOCK180

<400> 46
Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
1 5 10 15
Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
20 25 30
Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
35 40 45

<210> 47
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-1

<400> 47
Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala
1 5 10 15
Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys
20 25 30
Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg Gln
35 40 45
Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp
50 55

<210> 48
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from rat TRG

<400> 48
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala

Arg Tyr Phe Asp Asn Lys Val Lys Leu Ser Lys Gln Val Phe Arg Val
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 49
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human KIAA1058

<400> 49
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 50
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-2

<400> 50
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 51
<211> 58
<212> PRT
<213> Artificial Sequence

<400> 51

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 52

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and C from human CLASP-3

<400> 52

Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp
20 25 30

Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp
35 40 45

Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg
50 55

<210> 53

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP 4

<400> 53

Gln Leu Gln Leu Lys Leu Gln Gly Cys Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser
20 25 30

Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp Met Phe Arg Lys

<210> 54
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-5

<400> 54
Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln
1 5 10 15
Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp
20 25 30
Pro Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu
35 40 45
Phe Ile Met Arg Cys Gly Glu Ala Val Glu
50 55

<210> 55
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human KIAA0716

<400> 55
Pro Leu Thr Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
1 5 10 15
Gly Val Ser Arg Tyr Gln Glu Ala Phe Phe Val Lys Glu Tyr Ile Leu
20 25 30
Ser His Pro Glu Asp Gly Glu Lys Ile Ala Arg Leu Arg Glu Leu Met
35 40 45
Leu Glu Gln Ala Gln Ile Leu Glu Phe Gly Leu Ala
50 55 60

<210> 56
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from canonical DOCK2

Gly Ile Ala Lys Tyr Ser Lys Ala Thr Thr Thr Thr Thr Tyr Val Arg
20 25 30

Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu Ile
 35 40 45

Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys
 50 55 60

<210> 57
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from canonical DOCK3

<400> 57
 Leu Leu Ser Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
 1 5 10 15

Gly Ile Ala Arg Tyr Gln Glu Ala Phe Phe Asp Lys Asp Tyr Ile Asn
 20 25 30

Lys His Pro Gly Asp Ala Glu Lys Ile Thr Gln Leu Lys Glu Leu Met
 35 40 45

Gln Glu Gln Val His Val Leu Gly Val Gly Leu Ala
 50 55 60

<210> 58
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from canonical DOCK180

<400> 58
 Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
 1 5 10 15

Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
 20 25 30

Asp His Pro Glu Ala His Glu Lys Ile Glu Lys Leu Lys Asp Leu Ile
 35 40 45

Ala Trp Gln Ile Pro Phe Leu Ala Glu Gly Ile Arg
 50 55 60

<210> 59

<220>

<223> Description of Artificial Sequence:Ref 1.1
sequence of bacterial artificial chromosome BAC19
using primer HC5S11

<220>

<221> modified_base

<222> (1)..(598)

<223> n = g, a, c or t

<400> 59

```
ctctctgtct tcatatcttc caggttataa agnattatct actaaaagaa nattcangct 60
atttcatttta actagctcag tttaatcatg tatttcctat aaagggttagt cttattaatt 120
tgacaaaaca atcaaaacaat tcaaaccaga tcaagtatgc taccctgaag ttacaccact 180
agctaagaat taacaatcta agtaattggt ttctcccccag gctcaaggct cctgcatcag 240
gttaagtaaa gccaaagaat caataagccc tatgaaattt agaaactcat agaaaagtct 300
caaatcttct tgctcgacat tagccaattg ttatattatg caaatagagg atncaagta 360
aataagtttg gaacctgttt accagggtttt tgcagcagnc ctctaagagc ttaactggtc 420
atgcattgaa tgcagagagc aaagaggaat ggagaggggn tgtaagnggt tccaatntta 480
ctggaaccca ccactatctt tngaagtctt gatacttaac tngtgtagn ctctttaggc 540
ctntantaan tagaatctat atggattcgt gttctgtcng caagnagtgc ctatgaaa 598
```

<210> 60

<211> 625

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ref 2.1
sequence of bacterial artificial chromosome BAC19
using primer HC5AS10b

<220>

<221> modified_base

<222> (1)..(625)

<223> n = g, a, c or t

<400> 60

```
tgcgagtagt gtccgcgttc agcatgttgt actgcttata gggctgaagg gaggcacgat 60
tgggggatgg aggccaggga agaagtcaa caacagaaaa atttgaggct taacagtc aa 120
gcaacagaaa aattcaaagt gttctcttaa aataccatga ctgtacatca ctgctaggct 180
gagatctat tgcagtagc cctgccttcc ctaggcaggg gaagctgtgt tctttgagta 240
gagctactca gaaaagaggc tcacctgggg cagtatttga gctaggcttt cagccaccgt 300
atctgagtag ctctgtctta ngagcagtggt ggctgtgtga tcacctctgg gcttgatca 360
tgcgtgctgc aatcccgatg atacaaagag gctttcatgc tgctaagatc tccaagtatt 420
tctccttctg gctgggcagc agagggttag acttncaggg gagaaggaaa ctggctgggt 480
gcatgaata ancttgctgt tcaagantta acttctttgt tacataagng caaaggtata 540
acataaaggg ncatgaactg ctcaacnaaa ttatcaaat ccatgtttgt gggagttctt 600
ttgttatngg aagtttaacc cctaa 625
```

<210> 61

<211> 684

Sequence of Bacterial artificial chromosome BAC19
using primer C5S3

```
<221> modified_base
<222> (1)..(684)
<223> n = q, a, c or t
```

ccnngctctt	tttggaang	taancttggg	atgcttgttt	tcttctctct	aattaagagn	60
aagantcttt	ttagcttcat	actctctct	tcagggggac	caaaagtcac	agagcatatt	120
aagtggcana	accccaagg	ctttaagtct	tcctaggaag	aaagcagatg	ccctgattct	180
gtgggaagcc	accattggaga	ggaaaagcag	tggctcccat	atttgaagtg	nggacctaac	240
cttagaaagt	ttaaaanggc	catttgcctg	agggctatga	catgagaaca	gagatcaact	300
gagtgactta	gcaanttcac	cttttctctg	taanacctct	ggtgagtgag	antaaatcct	360
ntatgttagc	cccattagtc	ttacaaaang	tcatgcnta	aaatgccang	aaggncagaa	420
atgaattctt	caccgcgcga	ggaattgagg	ttatnctgtg	gggacatgca	naaatattnn	480
nccecnatt	tattnatta	tttattttgg	agacnagtn	tcgntctaat	cgccccagag	540
ctggnaggtg	gnaggtggtt	cccattctna	ancctanntn	ggaaggnccct	ctttgngccc	600
cnngggggng	naaangnaat	tcctataatg	ccctnanncc	cctccctgga	ngttatttgg	660
gqgnntnta	agggcngtg	gcng				684

```
<210> 62
<211> 450
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence:Ref 4.1
sequence of bacterial artificial chromosome BAC13
using primer C5S7
```

```
<220>
<221> modified_base
<222> (1)..(450)
<223> n = g, a, c or t
```

<400> 62						
acaaaaccta	accatcanc	tctaaatccc	aacaancttt	ttttaagaat	acctaangag	60
ctcaacnagg	gggactntcc	aangcactta	aatgcagnca	aacnacncn	ncaagagngg	120
caactactaa	tggggcanat	ctnaaagaaa	atatagncaa	aggngnga	cataatagga	180
cgacacactt	angaagcacc	aactggggac	ctgggaactgn	atnaggncct	ctacatacat	240
catnnnatan	catctctgaa	cgacccctgg	aggaganaag	anggnatttc	tannntagga	300
angaganaac	tggggacatg	ggaagaggna	agcgaagggt	tcaaggggna	gnaagcgagc	360
agannccagg	gnctcanact	ngngggggnnt	gggggggntnc	tgnnncccta	cncttngnan	420
gaacagcgnn	gttqanntgg	ctttnganta				450

```

c210: 63
c211: 502
c212: DNA
c213: Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 5.1
sequence of bacterial artificial chromosome BAC13

```

1. *Chlorophyll a* (Chl *a*)

<400> 63

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ccannagatt nttgnaacgn nggtaggctt cctttgtaga tttattgaaa atgtttcgta 60
cttctacaag tttgccctgc cttcctataa agagtgaan tcantttgaa tcgactgggtg 120
gataattntt ccatttttcc tcaggcaatt tngagttact ccaataaatt caaatatggg 180
ccagaggaaa tcctctttca gatgggcagt gattggccag tcagcaggag aagctgctta 240
tgcttggttt ggtacattgt ggaaaaacac actttaataa atacgcantc atgcttgagt 300
acccatcctc catcccgcga cccccagta tggcaaaaat ctggtcagag tccatttggg 360
aataattcca tggttcctgg gatcccaaaag cttccagaag tgctggctga tcaanggagt 420
gtacagtcag tcttgggtgg caaaaatgtc ccatttttta agtaccagac aaagggttct 480
tcttncaagg gttntcaggg cc 502
```

<210> 64

<211> 202

<212> DNA

<213> Homo sapiens

<220>

<223> 1st partial exon

<400> 64

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ccagctgcca gccaaagctca gtaaccttcc aacgctcatt tccatgaggc tagagtctct 60
gagaatcctc tgtagccatg agcattacct caatctgaac ctttttttta tgaatgctga 120
tactgctcca acatctcctt gtcttccat atcttcccag gtaataaaa aattatttaa 180
ctaaaagaat tattcaagct at 202
```

<210> 65

<211> 205

<212> DNA

<213> Homo sapiens

<220>

<223> 2nd exon

<400> 65

```
gtccataaaa tggtctctta cgtttctgta gaactcaagc tctgtctcca gttccagga 60
ccagaagatc gccagcatgt tcgatctgac ttccgagtag cgcagcagc acttctctac 120
cgggtctctc ttacagaaac tggtgtgtgc cctggatgcc gaaggggaag ggtatgtttc 180
tggcatttaa aatggaagat gaagc 205
```

<210> 66

<211> 235

<212> DNA

<213> Homo sapiens

<220>

<223> 3rd exon

<400> 66

```
cataacctct tgattcctgt gttgtgccc cagaatcagc aaagtacaaa ggaaagctgt 60
cagtgcaatt cacagcctgc taagttctca cgaactggac ccacgctgtg tcaaacagga 120
ggtgaaggtc aaaatcgccg cctttacct acctttagtt ggcacatctt tggatgcttt 180
```

<212> DNA

<213> Homo sapiens

<220>

<223> 4th exon

<400> 67

```
tgtttgactt gacatcacaa acgatgtttt cattgcagtt gcagatactc gcagataaccg 60
caccagtggc tcggatgaag aacaagaagg agccgggtgcc attaacccaga atgtggctct 120
ggccatagca gggaaataatt tcaatttgaa aacaagtgga atagtgtgtt cttccttggt 180
atgttggtgc acatgtgtct ggttgatttt tcac 214
```

<210> 68

<211> 247

<212> DNA

<213> Homo sapiens

<220>

<223> 5th exon

<400> 68

```
tggcctccat cccccaatct gcctcccttc agccctataa gcagtacaac atgctgaacg 60
cggacactac tcgcaacctc atgatctgct tcctctggat catgaaaaat gctgacaga 120
gcctcattag gaagtggatt gctgacctgc catcaacgca gctcaacagg attttagatc 180
tacttttcat ctgtgtgtta tgttttgagt ataaggttaag tctggagtgg cacaacttta 240
taccagc 247
```

<210> 69

<211> 205

<212> DNA

<213> Homo sapiens

<220>

<223> 6th exon

<400> 69

```
caccaaagga catgtctctc tacctctgtc ttgtccaggg aaaacagagt tctgacaaag 60
tcagtaccca agtctctcag aagtcagggt atgtcaaggc ccggctggaa gaggctttgc 120
tgcgtgggga aggggccaga ggggagatga tgcgccgccg ggctccaggt gtgttgact 180
ggccttccc tctctctgt caagc 205
```

<210> 70

<211> 156

<212> DNA

<213> Homo sapiens

<220>

<223> 7th exon

<400> 70

```
tcaaatctct atcatgcatt tcttaactcc tagggaacga ccgatttcca ggccataatg 60
aaaatttgag atggaagaaa gagcagacac attggcggca agctaagtag aagctagata 120
agtgaagcac tcggcaactt tctgtactt ttacct 156
```


<220>

<223> 8th exon

<400> 71

```
gctttaattt gacctcttgt tgtttcctag aacaaaggcc gagttagatc aagaagcctt 60
gatcagtggc aatctggcta cagaagcaca tttaatcacc ctggatatgc aggaaaacat 120
tatccaggtg aggaaaaaaa acaccaatc tgatttg 157
```

<210> 72

<211> 203

<212> DNA

<213> Homo sapiens

<220>

<223> 9th exon

<400> 72

```
ggattcaatg atgctgttct tccattcccc caggcgagct cggctctgga ctgtaaagac 60
agcctgctgg gaggtgttct gagggtgctg gtgaattctc tgaactgtga tcagagtacc 120
acctacctga ctactgctt tgcaacactc cgtgctctca tcgccaaggt aaacttggga 180
tgcttgtttt ctctctctta att 203
```

<210> 73

<211> 223

<212> DNA

<213> Homo sapiens

<220>

<223> 10th exon

<400> 73

```
agtgatgcct aatggccctt tatgtctctc ctagtgttga gacttactct tcgaagagga 60
ggtggaacag tgtttcgacc tatgtcacca agtctctcac cactgcagca gcagcatgga 120
tgtcaccccg agccaagcct gtgccaccct ttacctctc atgaggttca gttttggagc 180
caccagtgtg agagttcaaa ccagctgagt gacctggaat cag 223
```

<210> 74

<211> 230

<212> DNA

<213> Homo sapiens

<220>

<223> 11th exon

<400> 74

```
ttacttcacc tttttttttt ttttctactga tgcagaattt tgcaagagta aagatgcaag 60
taaccatgtc cctggcatct ttgggtggaa gagcaccaga ctttaatgaa gagcacctga 120
gaagatcctt gaggacaatt ttggcctatt cagaagagga cacagccatg cagatgactc 180
cttttccac ccaggtacac cgaagcacat accttgtctc atgcatgagt 230
```

<220>

<223> 12th exon

<400> 75

agctaagatt attttgaggc ttacactttt tgcagggtgga ggaacttctc tgtaattctga 60
atagcatctt atatgacaca gtgaaaatga ggggaatttca ggaagatcct gagatgctta 120
tggatctcat gtacaggtaa gcttttctga cacactcaag ggacaccatt t 171

<210> 76

<211> 266

<212> DNA

<213> Homo sapiens

<220>

<223> 13th exon

<400> 76

tcttcaaaac tactttctac tcaatctgtc ttcagaattg ccaagagtta ccaggcatct 60
cctgatctgc ggctgacctg gctccagaac atggcagaga aacacaccaa gaagaagtgc 120
tacacggagg ctgccatgtg cctgggtgcac gccgctgcgt tagtggtgta gtatctgagc 180
atgctggagg accacagcta cctgccctg ggcagtgtca gcttccaggt aggggtgtgtg 240
cagcttttcc cttagagcag tggttc 266

<210> 77

<211> 211

<212> DNA

<213> Homo sapiens

<220>

<223> 14th exon

<400> 77

ctgtttctca ggcttatact gtgggtctct tcagaatatt tcttccaatg tgctggagga 60
gtctgtggtc tctgaggaca cctgtcacc tgacgaggat ggggtgtgcg caggccagta 120
cttcaccgag agtggcctgg taggcctcct ggagcaggcc gcggagctct tcagcacggt 180
cagtgccag agggcatccc ggggcctggc c 211

<210> 78

<211> 199

<212> DNA

<213> Homo sapiens

<220>

<223> 15th exon

<400> 78

aattctctct gatgetcttc tctcttttcc aaggaggagct tatatgagac agttaatgag 60
gtctacaagc tggtcacccc catctagaa gcgcacagag aattccggaa gctgacactc 120
actcacagca agctgcagag agccttcgac agcatcgta acaaggtagc cggggagcct 180
ggctggcagg tcttggtac 199

<210> 79

<211> 208

<400> 79

```
taaggagagc tttttatatt ttgttctca ggatcataag agaattgttg gaacctactt 60
ccgagtttgt ttttttgat ccaaatttgg ggatttggat gaacaggagt ttgtctacaa 120
agagcctgca attaccaagc ttcttgagat ctcacataga ctagaggtaa gaaaagtgt 180
tctgtgcgcc tgacctggta cactttac 208
```

<210> 80

<211> 157

<212> DNA

<213> Homo sapiens

<220>

<223> 17th exon

<400> 80

```
aacctttata aactgttggt ttttcttacc taggcatttt atgggtcaatg ttttggtgca 60
gaattttgtgg aagtgtattaa agactccact cctgtggaca aaaccaagtt ggatcctaac 120
aagglataca aaaatttaca aaaactaacc atcaagc 157
```

<210> 81

<211> 304

<212> DNA

<213> Homo sapiens

<220>

<223> 18th exon

<400> 81

```
tcttctccct cngtgccttt tcccccttag gctacatac agatcacttt tgtggagccc 60
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<212> DNA

<213> Homo sapiens

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<223> putative human CLASP-5 promoter

<400> 87

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35 40 45
Val Val Asn Tyr Lys Tyr Glu Asp Phe Ser Gly Asp Phe Arg Met Leu
50 55 60
Pro Cys Lys Ser Leu Arg Pro Glu Lys Ile Pro Asn His Val Phe Glu
65 70 75 80
Ile Asp Glu Asp Cys Glu Lys Asp Glu Asp Ser Ser Ser Leu Cys Ser
85 90 95
Gln Lys Gly Gly Val Ile Lys Gln Gly Trp Leu His Lys Ala Asn Val
100 105 110
Asn Ser Thr Ile Thr Val Thr Met Lys Val Phe Lys Arg Arg Tyr Phe
115 120 125
Tyr Leu Thr Gln Leu Pro Asp Gly Ser Tyr Ile Leu Asn Ser Tyr Lys
130 135 140
Asp Glu Lys Asn Ser Lys Glu Ser Lys Gly Cys Ile Tyr Leu Asp Ala
145 150 155 160
Cys Ile Asp Val Val Gln Cys Pro Lys Met Arg Arg His Ala Phe Glu
165 170 175
Leu Lys Met Leu Asp Lys Tyr Ser His Tyr Leu Ala Ala Glu Thr Glu
180 185 190
Gln Glu Met Glu Glu Trp Leu Ile Thr Leu Lys Lys Ile Ile Gln Ile
195 200 205
Asn Thr Asp Ser Leu Val Gln Glu Lys Lys Glu Thr Val Glu Thr Ala
210 215 220
Gln Asp Asp Glu Thr Ser Ser Gln Gly Lys Ala Glu Asn Ile Met Ala
225 230 235 240

Phe Ser Phe Asp Ser Glu Val Gln Arg Leu Asp Phe Ser Gly Ile Glu
275 280 285

Pro Asp Ile Lys Pro Phe Glu Glu Lys Cys Asn Lys Arg Phe Leu Val
290 295 300

Asn Cys His Asp Leu Thr Phe Asn Ile Leu Gly Gln Ile Gly Asp Asn
305 310 315 320

Ala Lys Gly Pro Pro Thr Asn Val Glu Pro Phe Phe Ile Asn Leu Ala
325 330 335

Leu Phe Asp Val Lys Asn Asn Cys Lys Ile Ser Ala Asp Phe His Val
340 345 350

Asp Leu Asn Pro Pro Ser Val Arg Glu Met Leu Trp Gly Ser Ser Thr
355 360 365

Gln Leu Ala Ser Asp Gly Ser Pro Lys Gly Ser Ser Pro Glu Ser Tyr
370 375 380

Ile His Gly Ile Ala Glu Ser Gln Leu Arg Tyr Ile Gln Gln Gly Ile
385 390 395 400

Phe Ser Val Thr Asn Pro His Pro Glu Ile Phe Leu Val Ala Arg Ile
405 410 415

Glu Lys Val Leu Gln Gly Asn Ile Thr His Cys Ala Glu Pro Tyr Ile
420 425 430

Lys Asn Ser Asp Pro Val Lys Thr Ala Gln Lys Val His Arg Thr Ala
435 440 445

Lys Gln Val Cys Ser Arg Leu Gly Gln Tyr Arg Met Pro Phe Ala Trp
450 455 460

Ala Ala Arg Pro Ile Phe Lys Asp Thr Gln Gly Ser Leu Asp Leu Asp
465 470 475 480

Gly Arg Phe Ser Pro Leu Tyr Lys Gln Asp Ser Ser Lys Leu Ser Ser
485 490 495

Glu Asp Ile Leu Lys Leu Leu Ser Glu Tyr Lys Lys Pro Glu Lys Thr
500 505 510

Lys Leu Gln Ile Ile Pro Gly Gln Leu Asn Ile Thr Val Glu Cys Val
515 520 525

Pro Val Asp Leu Ser Asn Cys Ile Thr Ser Ser Tyr Val Pro Leu Lys
530 535 540

Pro Phe Glu Lys Asn Cys Gln Asn Ile Thr Val Glu Val Glu Glu Phe
545 550 555 560

Phe	Ala	Lys	Ala	Arg	Asn	Ile	Ala	Val	Cys	Val	Glu	Phe	Arg	Asp	Ser	595	600	605
Asp	Glu	Ser	Asp	Ala	Ser	Ala	Leu	Lys	Cys	Ile	Tyr	Gly	Lys	Pro	Ala	610	615	620
Gly	Ser	Val	Phe	Thr	Thr	Asn	Ala	Tyr	Ala	Val	Val	Ser	His	His	Asn	625	630	635
Gln	Asn	Pro	Glu	Phe	Tyr	Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Ile	His	645	650	655
Leu	His	Gln	Lys	His	His	Leu	Leu	Phe	Thr	Phe	Tyr	His	Val	Ser	Cys	660	665	670
Glu	Ile	Asn	Thr	Lys	Gly	Thr	Thr	Lys	Lys	Gln	Asp	Thr	Val	Glu	Thr	675	680	685
Pro	Val	Gly	Phe	Ala	Trp	Val	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Ile	Ile	690	695	700
Thr	Phe	Glu	Gln	Gln	Leu	Pro	Val	Ser	Ala	Asn	Leu	Pro	Pro	Gly	Tyr	705	710	715
Leu	Asn	Leu	Asn	Asp	Ala	Glu	Ser	Arg	Arg	Gln	Cys	Asn	Val	Asp	Ile	725	730	735
Lys	Trp	Val	Asp	Gly	Ala	Lys	Pro	Leu	Leu	Lys	Phe	Lys	Ser	His	Leu	740	745	750
Glu	Ser	Thr	Ile	Tyr	Thr	Gln	Asp	Leu	His	Val	His	Lys	Phe	Phe	His	755	760	765
His	Cys	Gln	Leu	Ile	Gln	Ser	Gly	Ser	Lys	Glu	Val	Pro	Gly	Glu	Leu	770	775	780
Ile	Lys	Tyr	Leu	Lys	Cys	Leu	His	Ala	Met	Glu	Ile	Gln	Val	Met	Ile	785	790	795
Gln	Phe	Leu	Pro	Val	Ile	Leu	Met	Gln	Leu	Phe	Arg	Val	Leu	Thr	Asn	805	810	815
Met	Thr	His	Glu	Asp	Asp	Val	Pro	Ile	Asn	Cys	Thr	Met	Val	Leu	Leu	820	825	830
His	Ile	Val	Ser	Lys	Cys	His	Glu	Gly	Leu	Asp	Ser	Tyr	Leu	Arg		835	840	845
Ser	Phe	Ile	Lys	Tyr	Ser	Phe	Arg	Pro	Glu	Lys	Pro	Ser	Ala	Pro	Gln	850	855	860
Ala	Gln	Leu	Ile	His	Glu	Thr	Leu	Ala	Thr	Thr	Met	Ile	Ala	Ile	Leu	865	870	875

Glu Glu Asn Lys Ile Lys Leu Pro Arg Gly Gln Arg Phe Pro Glu Thr
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 Tyr His His Val Leu His Ser Leu Leu Leu Ala Ile Ile Pro His Val
 930 935 940
 Thr Ile Arg Tyr Ala Glu Ile Pro Asp Glu Ser Arg Asn Val Asn Tyr
 945 950 955 960
 Ser Leu Ala Ser Phe Leu Lys Arg Cys Leu Thr Leu Met Asp Arg Gly
 965 970 975
 Phe Ile Phe Asn Leu Ile Asn Asp Tyr Ile Ser Gly Phe Ser Pro Lys
 980 985 990
 Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe Glu Phe Leu Gln Thr Ile
 995 1000 1005
 Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro Met Ala Phe Ala
 1010 1015 1020
 Lys Pro Lys Leu Gln Arg Val Gln Asp Ser Asn Leu Glu Tyr Ser Leu
 1025 1030 1035 1040
 Ser Asp Glu Tyr Cys Lys His His Phe Leu Val Gly Leu Leu Leu Arg
 1045 1050 1055
 Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr Glu Ile Arg Tyr Thr Ala
 1060 1065 1070
 Ile Ser Val Ile Lys Asn Leu Leu Ile Lys His Ala Phe Asp Thr Arg
 1075 1080 1085
 Tyr Gln His Lys Asn Gln Gln Ala Lys Ile Ala Gln Leu Tyr Leu Pro
 1090 1095 1100
 Phe Val Gly Leu Leu Leu Glu Asn Ile Gln Arg Leu Ala Gly Arg Asp
 1105 1110 1115 1120
 Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn Ser Ala Ser Arg Asp Glu
 1125 1130 1135
 Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn Arg Gly Ser Leu Ser Thr
 1140 1145 1150
 Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln Asn Gly His Gly Ile Lys
 1155 1160 1165
 Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro Glu Gly Ala Thr Gly Phe
 1170 1175 1180
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 1185 1190 1195 1200

Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro Gln Glu Leu Ile Asn Ile
 1235 1240 1245
 Leu Ile Leu Leu Glu Val Cys Leu Phe His Phe Arg Tyr Met Gly Lys
 1250 1255 1260
 Arg Asn Ile Ala Arg Val His Asp Ala Trp Leu Ser Lys His Phe Gly
 1265 1270 1275 1280
 Ile Asp Arg Lys Ser Gln Thr Met Pro Ala Leu Arg Asn Arg Ser Gly
 1285 1290 1295
 Val Met Gln Ala Arg Leu Gln His Leu Ser Ser Leu Glu Ser Ser Phe
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 Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn Glu Ala Ser Ala Leu Leu
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 Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr Thr Lys Arg Lys Thr Phe
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Arg Lys Thr Trp Leu Asp Ser Met Ala Lys Ile His Val Lys Asn Gly
 1555 1560 1565

Asp Phe Ser Glu Ala Ala Met Cys Tyr Val His Val Ala Ala Leu Val
 1570 1575 1580

Ala Glu Phe Leu His Arg Lys Lys Leu Phe Pro Asn Gly Cys Ser Ala
 1585 1590 1595 1600

Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu Glu Gly Ala Met Lys Glu
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Asp Ala Gly Met Met Asp Val His Tyr Ser Glu Glu Val Leu Leu Glu
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Leu Leu Glu Gln Cys Val Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu
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Ile Ile Ser Glu Ile Ser Lys Leu Ile Val Pro Ile Tyr Glu Lys Arg
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Arg Glu Phe Glu Lys Leu Thr Gln Val Tyr Arg Thr Leu His Gly Ala
 1665 1670 1675 1680

Tyr Thr Lys Ile Leu Glu Val Met His Thr Lys Lys Arg Leu Leu Gly
 1685 1690 1695

Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu
 1700 1705 1710

Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser
 1715 1720 1725

Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr Gly Glu Lys Phe Gly Thr
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Glu Asn Val Lys Ile Ile Gln Asp Ser Asp Lys Val Asn Ala Lys Glu
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Leu Asp Pro Lys Tyr Ala His Ile Gln Val Thr Tyr Val Lys Pro Tyr
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Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys Thr Glu Phe Glu Arg Asn
 1780 1785 1790

His Asn Ile Ser Arg Phe Val Phe Glu Ala Pro Tyr Thr Leu Ser Gly
 1795 1800 1805

Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu
 1810 1815 1820

Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg Ile Pro Ile Asn
 1825 1830 1835 1840

Val Asp Met Ile Gln Leu Gln Leu Lys Leu Gln Gly Trp Val Ser Val
1875 1880 1885

Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp
1890 1895 1900

Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp
1905 1910 1915 1920

Met Phe Arg Lys Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu Leu Asn
1925 1930 1935

Glu Arg Leu Ile Lys Glu Asp Gln Val Glu Tyr His Glu Gly Leu Lys
1940 1945 1950

Ser Asn Phe Arg Asp Met Val Lys Glu Leu Ser Asp Ile Ile His Glu
1955 1960 1965

Gln Ile Leu Gln Glu Asp Thr Met His Ser Pro Trp Met Ser Asn Thr
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Leu His val Phe Cys Ala Ile Ser Gly Thr Ser Ser Asp Arg Gly Tyr
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Gly Ser Pro Arg Tyr Ala Glu Val
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<223> human CLASP-5

<400> 89

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Arg Thr Leu Gln Pro Ser Leu Pro Glu Glu Gly Val Glu Leu Asp Pro
35 40 45

His Val Arg Asp Cys Val Gln Thr Tyr Ile Arg Glu Trp Leu Ile Val
50 55 60

Asn Arg Lys Asn Gln Gly Ser Pro Glu Ile Cys Gly Phe Lys Lys Thr
65 70 75 80

Gly Ser Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu
85 90 95

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145					150					155					160
Ala	Arg	Arg	Thr	Asn	Arg	Gln	Ala	Glu	Leu	Phe	Ala	Leu	Tyr	Pro	Ser
				165					170					175	
Val	Asp	Glu	Glu	Asp	Ala	Val	Glu	Ile	Arg	Pro	Val	Pro	Glu	Cys	Pro
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		195					200					205			
Phe	Glu	Ile	Glu	Ile	Glu	Pro	Leu	Phe	Ala	Ser	Ile	Ala	Leu	Tyr	Asp
		210				215					220				
Val	Lys	Glu	Arg	Lys	Lys	Ile	Ser	Glu	Asn	Phe	His	Cys	Asp	Leu	Asn
225					230					235					240
Ser	Asp	Gln	Phe	Lys	Gly	Phe	Leu	Arg	Ala	His	Thr	Pro	Ser	Val	Ala
				245					250					255	
Ala	Ser	Ser	Gln	Ala	Arg	Ser	Ala	Val	Phe	Ser	Val	Thr	Tyr	Pro	Ser
			260					265						270	
Ser	Asp	Ile	Tyr	Leu	Val	Val	Lys	Ile	Glu	Lys	Val	Leu	Gln	Gln	Gly
		275					280					285			
Asp	Ile	Gly	Asp	Cys	Ala	Glu	Pro	Tyr	Thr	Val	Ile	Lys	Glu	Ser	Asp
	290					295					300				
Gly	Gly	Lys	Ser	Lys	Glu	Lys	Ile	Glu	Lys	Leu	Lys	Leu	Gln	Ala	Glu
305					310					315					320
Ser	Phe	Cys	Gln	Arg	Leu	Gly	Lys	Tyr	Arg	Met	Pro	Phe	Ala	Trp	Ala
				325					330					335	
Pro	Ile	Ser	Leu	Ser	Ser	Phe	Phe	Asn	Val	Ser	Thr	Leu	Glu	Arg	Glu
			340					345						350	
Val	Thr	Asp	Val	Asp	Ser	Val	Val	Gly	Arg	Ser	Pro	Val	Gly	Glu	Arg
		355					360					365			
Arg	Thr	Leu	Ala	Gln	Ser	Arg	Arg	Leu	Ser	Glu	Arg	Ala	Leu	Ser	Leu
		370				375					380				
Glu	Glu	Asn	Gly	Val	Gly	Ser	Asn	Phe	Lys	Thr	Ser	Thr	Leu	Ser	Val
385					390					395					400
Ser	Ser	Phe	Phe	Lys	Gln	Glu	Gly	Asp	Arg	Leu	Ser	Asp	Glu	Asp	Leu
				405					410					415	

Glu Ile Ile Asn Cys Cys Leu Thr Pro Glu Met Leu Pro Val Lys Pro	450	455	460
Phe Pro Glu Asn Arg Thr Arg Pro His Lys Glu Ile Leu Glu Phe Pro	465	470	475
Thr Arg Glu Val Tyr Val Pro His Thr Val Tyr Arg Asn Leu Leu Tyr	485	490	495
Val Tyr Pro Gln Arg Leu Asn Phe Val Asn Lys Leu Ala Ser Ala Arg	500	505	510
Asn Ile Thr Ile Lys Ile Gln Phe Met Cys Gly Glu Asp Ala Ser Asn	515	520	525
Ala Met Pro Val Ile Phe Gly Lys Ser Ser Gly Pro Glu Phe Leu Gln	530	535	540
Glu Val Tyr Thr Ala Val Thr Tyr His Asn Lys Ser Pro Asp Phe Tyr	545	550	555
Glu Glu Val Lys Ile Lys Leu Pro Ala Lys Leu Thr Val Asn His His	565	570	575
Leu Leu Phe Thr Phe Tyr His Ile Ser Cys Gln Gln Lys Gln Gly Ala	580	585	590
Ser Val Glu Thr Leu Leu Gly Tyr Ser Trp Leu Pro Ile Leu Leu Asn	595	600	605
Glu Arg Leu Gln Thr Gly Ser Tyr Cys Leu Pro Val Ala Leu Glu Lys	610	615	620
Leu Pro Pro Asn Tyr Ser Met His Ser Ala Glu Lys Val Pro Leu Gln	625	630	635
Asn Pro Pro Ile Lys Trp Ala Glu Gly His Lys Gly Val Phe Asn Ile	645	650	655
Glu Val Gln Ala Val Ser Ser Val His Thr Gln Asp Asn His Leu Glu	660	665	670
Lys Phe Phe Thr Leu Cys His Ser Leu Glu Ser Gln Val Thr Phe Pro	675	680	685
Ile Arg Val Leu Asp Gln Lys Ile Ser Glu Met Ala Leu Glu His Glu	690	695	700
Leu Lys Leu Ser Ile Ile Cys Leu Asn Ser Ser Arg Leu Glu Pro Leu	705	710	715
Val Leu Phe Leu His Leu Val Leu Asp Lys Leu Phe Gln Leu Ser Val	725	730	735

Leu	Ser	Lys	Asp	Gln	His	Gly	Arg	Asn	Cys	Leu	Leu	Ala	Ser	Tyr	Val
770						775					780				
His	Tyr	Val	Phe	Arg	Leu	Pro	Glu	Val	Gln	Arg	Asp	Val	Pro	Lys	Ser
785					790					795					800
Gly	Ala	Pro	Thr	Ala	Leu	Leu	Asp	Pro	Arg	Ser	Tyr	His	Thr	Tyr	Gly
				805					810					815	
Arg	Thr	Ser	Ala	Ala	Ala	Val	Ser	Ser	Lys	Leu	Leu	Gln	Ala	Arg	Val
			820					825					830		
Met	Ser	Ser	Ser	Asn	Pro	Asp	Leu	Ala	Gly	Thr	His	Ser	Ala	Ala	Asp
	835						840					845			
Glu	Glu	Val	Lys	Asn	Ile	Met	Ser	Ser	Lys	Ile	Ala	Asp	Arg	Asn	Cys
850					855						860				
Ser	Arg	Met	Ser	Tyr	Tyr	Cys	Ser	Gly	Ser	Ser	Asp	Ala	Pro	Ser	Ser
865					870					875					880
Pro	Ala	Ala	Pro	Arg	Pro	Ala	Ser	Lys	Lys	His	Phe	His	Glu	Glu	Leu
				885					890					895	
Ala	Leu	Gln	Met	Val	Val	Ser	Thr	Gly	Met	Val	Lys	Ser	Met	Ala	Gln
			900					905					910		
His	Val	His	Asn	Met	Asp	Lys	Arg	Asp	Ser	Phe	Arg	Arg	Thr	Arg	Phe
	915						920					925			
Ser	Asp	Arg	Phe	Met	Asp	Asp	Ile	Thr	Thr	Ile	Val	Asn	Val	Val	Thr
	930					935					940				
Ser	Glu	Ile	Ala	Ala	Leu	Leu	Val	Lys	Pro	Gln	Lys	Glu	Asn	Glu	Gln
945					950					955					960
Ala	Glu	Lys	Met	Asn	Ile	Ser	Leu	Ala	Phe	Phe	Leu	Tyr	Asp	Leu	Leu
				965					970					975	
Ser	Leu	Met	Asp	Arg	Gly	Phe	Val	Phe	Asn	Leu	Ile	Arg	His	Tyr	Cys
			980					985					990		
Ser	Gln	Leu	Ser	Ala	Lys	Leu	Ser	Asn	Leu	Pro	Thr	Leu	Ile	Ser	Met
	995						1000					1005			
Arg	Leu	Glu	Phe	Leu	Arg	Ile	Leu	Cys	Ser	His	Glu	His	Tyr	Leu	Asn
	1010				1015						1020				
Leu	Asn	Leu	Phe	Phe	Met	Asn	Ala	Asp	Thr	Ala	Pro	Thr	Ser	Pro	Cys
1025					1030					1035				1040	
Pro	Ser	Ile	Ser	Ser	Gln	Asn	Ser	Ser	Ser	Cys	Ser	Ser	Phe	Gln	Asp
			1045					1050					1055		

Ala Glu Gly Glu Gly Ile Ser Lys Val Gln Arg Lys Ala Val Ser Ala
1090 1095 1100

Ile His Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys
1105 1110 1115 1120

Pro Glu Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly
1125 1130 1135

Ile Ile Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp
1140 1145 1150

Thr Arg Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala
1155 1160 1165

Gly Ala Ile Asn Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe
1170 1175 1180

Asn Leu Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln
1185 1190 1195 1200

Tyr Asn Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe
1205 1210 1215

Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile
1220 1225 1230

Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe
1235 1240 1245

Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys
1250 1255 1260

Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu
1265 1270 1275 1280

Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg
1285 1290 1295

Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu
1300 1305 1310

Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu
1315 1320 1325

Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn
1330 1335 1340

Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile
1345 1350 1355 1360

Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly
1365 1370 1375

Gly Asp Leu Leu Phe	Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys
1410	1415 1420
His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser	
1425	1430 1435 1440
Gln Ala Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala	
1445	1450 1455
Thr Ser Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala	
1460	1465 1470
Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg	
1475	1480 1485
Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln	
1490	1495 1500
Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn	
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Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro	
1525	1530 1535
Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala	
1540	1545 1550
Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His	
1555	1560 1565
Thr Lys Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala	
1570	1575 1580
Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr	
1585	1590 1595 1600
Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu	
1605	1610 1615
Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly	
1620	1625 1630
Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu	
1635	1640 1645
Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val	
1650	1655 1660
Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu	
1665	1670 1675 1680
Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp	
1685	1690 1695

Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg
 1730 1735 1740

Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val
 1745 1750 1755 1760

Ile Lys Asp Ser Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys
 1765 1770 1775

Ala Tyr Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu
 1780 1785 1790

Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg
 1795 1800 1805

Phe Met Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu
 1810 1815 1820

Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala
 1825 1830 1835 1840

Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe
 1845 1850 1855

Val Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr
 1860 1865 1870

Leu Gln Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met
 1875 1880 1885

Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly
 1890 1895 1900

Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro
 1905 1910 1915 1920

Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe
 1925 1930 1935

Ile Met Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr
 1940 1945 1950

Ala Asp Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys
 1955 1960 1965

Leu Lys Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu
 1970 1975 1980

Tyr Lys Pro Ile Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His
 1985 1990 1995 2000

Arg Ser Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
 2005 2010 2015

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<223> human CLASP-3

<400> 90

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Ala Glu Val Arg Lys Gln Ile Ser Gly Gln Tyr Ser Gly Ser Pro Gln
20 25 30

Leu Leu Lys Asn Leu Asn Ile Val Gly Asn Ile Ser His His Thr Thr
35 40 45

Val Pro Leu Thr Glu Ala Val Asp Pro Val Asp Leu Glu Asp Tyr Leu
50 55 60

Ile Thr His Pro Leu Ala Val Asp Ser Gly Pro Leu Arg Asp Leu Ile
65 70 75 80

Glu Phe Pro Pro Asp Asp Ile Glu Val Val Tyr Ser Pro Arg Asp Cys
85 90 95

Arg Thr Leu Val Ser Ala Val Pro Glu Glu Ser Glu Met Asp Pro His
100 105 110

Val Arg Asp Cys Ile Arg Ser Tyr Thr Glu Asp Trp Ala Ile Val Ile
115 120 125

Arg Lys Tyr His Lys Leu Gly Thr Gly Phe Asn Pro Asn Thr Leu Asp
130 135 140

Lys Gln Lys Glu Arg Gln Lys Gly Leu Pro Lys Gln Val Phe Glu Ser
145 150 155 160

Asp Glu Ala Pro Asp Gly Asn Ser Tyr Gln Asp Asp Gln Asp Asp Leu
165 170 175

Lys Arg Arg Ser Met Ser Ile Asp Asp Thr Pro Arg Gly Ser Trp Ala
180 185 190

Cys Ser Ile Phe Asp Leu Lys Asn Ser Leu Pro Asp Ala Leu Leu Pro
195 200 205

Asn Leu Leu Asp Arg Thr Pro Asn Glu Glu Ile Asp Arg Gln Asn Asp
210 215 220

Asp Gln Arg Lys Ser Asn Arg His Lys Glu Leu Phe Ala Leu His Pro
225 230 235 240

Ser Pro Asp Glu Glu Glu Pro Ile Glu Arg Leu Ser Val Pro Asp Ile
245 250 255

Pro Lys Glu His Phe Gly Gln Arg Leu Leu Val Lys Cys Leu Ser Leu
260 265 270

Arg Val Lys Ile Lys Lys Asp Leu Val Ala Ala Val Lys Val His Val
280 285 290

Asn	Ser	Glu	Gln	Met	Lys	Gly	Leu	Leu	Arg	Pro	His	Val	Pro	Pro	Ala
305					310					315					320
Ala	Ile	Thr	Thr	Leu	Ala	Arg	Ser	Ala	Ile	Phe	Ser	Ile	Thr	Tyr	Pro
				325					330					335	
Ser	Gln	Asp	Val	Phe	Leu	Val	Ile	Lys	Leu	Glu	Lys	Val	Leu	Gln	Gln
			340					345					350		
Gly	Asp	Ile	Gly	Glu	Cys	Ala	Glu	Pro	Tyr	Met	Ile	Phe	Lys	Glu	Ala
		355					360					365			
Asp	Ala	Thr	Lys	Asn	Lys	Glu	Lys	Leu	Glu	Lys	Leu	Lys	Ser	Gln	Ala
	370					375						380			
Asp	Gln	Phe	Cys	Gln	Arg	Leu	Gly	Lys	Tyr	Arg	Met	Pro	Phe	Ala	Trp
385					390					395					400
Thr	Ala	Ile	His	Leu	Met	Asn	Ile	Val	Ser	Ser	Ala	Gly	Ser	Leu	Glu
				405					410					415	
Arg	Asp	Ser	Thr	Glu	Val	Glu	Ile	Ser	Thr	Gly	Glu	Arg	Lys	Gly	Ser
			420						425				430		
Trp	Ser	Glu	Arg	Arg	Asn	Ser	Ser	Ile	Val	Gly	Arg	Arg	Ser	Leu	Glu
		435					440					445			
Arg	Thr	Thr	Ser	Gly	Asp	Asp	Ala	Cys	Asn	Leu	Thr	Ser	Phe	Arg	Pro
	450					455						460			
Ala	Thr	Leu	Thr	Val	Thr	Asn	Phe	Phe	Lys	Gln	Glu	Gly	Asp	Arg	Leu
465					470					475					480
Ser	Asp	Glu	Asp	Leu	Tyr	Lys	Phe	Leu	Ala	Asp	Met	Arg	Arg	Pro	Ser
				485					490					495	
Ser	Val	Leu	Arg	Arg	Leu	Arg	Pro	Ile	Thr	Ala	Gln	Leu	Lys	Ile	Asp
			500					505					510		
Ile	Ser	Pro	Ala	Pro	Glu	Asn	Pro	His	Tyr	Cys	Leu	Thr	Pro	Glu	Leu
		515					520					525			
Leu	Gln	Val	Lys	Leu	Tyr	Pro	Asp	Ser	Arg	Val	Arg	Pro	Thr	Arg	Glu
		530				535					540				
Ile	Leu	Glu	Phe	Pro	Ala	Arg	Asp	Val	Tyr	Val	Pro	Asn	Thr	Thr	Tyr
545				550					555						560
Arg	Asn	Leu	Leu	Tyr	Ile	Tyr	Pro	Gln	Ser	Leu	Asn	Phe	Ala	Asn	Arg
				565				570					575		
Gln	Gly	Ser	Ala	Arg	Asn	Ile	Thr	Val	Lys	Val	Gln	Phe	Met	Tyr	Gly
			580				585						590		

Ser	Pro	Asp	Phe	His	Glu	Glu	Ile	Lys	Val	Lys	Leu	Pro	Ala	Thr	Leu	625	630	635	640
Thr	Asp	His	His	His	Leu	Leu	Phe	Thr	Phe	Tyr	His	Val	Ser	Cys	Gln	645	650	655	
Gln	Lys	Gln	Asn	Thr	Pro	Leu	Glu	Thr	Pro	Val	Gly	Tyr	Thr	Trp	Ile	660	665	670	
Pro	Met	Leu	Gln	Asn	Gly	Arg	Leu	Lys	Thr	Gly	Gln	Phe	Cys	Leu	Pro	675	680	685	
Val	Ser	Leu	Glu	Lys	Pro	Pro	Gln	Ala	Tyr	Ser	Val	Leu	Ser	Pro	Glu	690	695	700	
Val	Pro	Leu	Pro	Gly	Met	Lys	Trp	Val	Asp	Asn	His	Lys	Gly	Val	Phe	705	710	715	720
Asn	Val	Glu	Val	Val	Ala	Val	Ser	Ser	Ile	His	Thr	Gln	Asp	Pro	Tyr	725	730	735	
Leu	Asp	Lys	Phe	Phe	Ala	Leu	Val	Asn	Ala	Leu	Asp	Glu	His	Leu	Phe	740	745	750	
Pro	Val	Arg	Ile	Gly	Asp	Met	Arg	Ile	Met	Glu	Asn	Asn	Leu	Glu	Asn	755	760	765	
Glu	Leu	Lys	Ser	Ser	Ile	Ser	Ala	Leu	Asn	Ser	Ser	Gln	Leu	Glu	Pro	770	775	780	
Val	Val	Arg	Phe	Leu	His	Leu	Leu	Leu	Asp	Lys	Leu	Ile	Leu	Leu	Val	785	790	795	800
Ile	Arg	Pro	Pro	Val	Ile	Ala	Gly	Gln	Ile	Val	Asn	Leu	Gly	Gln	Ala	805	810	815	
Ser	Phe	Glu	Ala	Met	Ala	Ser	Ile	Ile	Asn	Arg	Leu	His	Lys	Asn	Leu	820	825	830	
Glu	Gly	Asn	His	Asp	Gln	His	Gly	Arg	Asn	Ser	Leu	Leu	Ala	Ser	Tyr	835	840	845	
Ile	His	Tyr	Val	Phe	Arg	Leu	Pro	Asn	Thr	Tyr	Pro	Asn	Ser	Ser	Ser	850	855	860	
Pro	Gly	Pro	Gly	Gly	Leu	Gly	Gly	Ser	Val	His	Tyr	Ala	Thr	Met	Ala	865	870	875	880
Arg	Ser	Ala	Val	Arg	Pro	Ala	Ser	Leu	Asn	Leu	Asn	Arg	Ser	Arg	Ser	885	890	895	
Leu	Ser	Asn	Ser	Asn	Pro	Asp	Ile	Ser	Gly	Thr	Pro	Thr	Ser	Pro	Asp	900	905	910	

Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala Met Asp Arg Ser Cys Asn	945	950	955	960
Arg Met Ser Ser His Thr Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr		965	970	975
Gly Arg Leu Pro Thr Lys Lys Leu Phe His Glu Glu Leu Ala Leu Gln		980	985	990
Trp Val Val Cys Ser Gly Ser Val Arg Glu Ser Ala Leu Gln Gln Ala		995	1000	1005
Trp Phe Phe Phe Glu Leu Met Val Lys Ser Met Val His His Leu Tyr		1010	1015	1020
Phe Asn Asp Lys Leu Glu Ala Pro Arg Lys Ser Arg Phe Pro Glu Arg		1025	1030	1035
Phe Met Asp Asp Ile Ala Ala Leu Val Ser Thr Ile Ala Ser Asp Ile		1045	1050	1055
Val Ser Arg Phe Gln Lys Asp Thr Glu Met Val Glu Arg Leu Asn Thr		1060	1065	1070
Ser Leu Ala Phe Phe Leu Asn Asp Leu Leu Ser Val Met Asp Arg Gly		1075	1080	1085
Phe Val Phe Ser Leu Ile Lys Ser Cys Tyr Lys Gln Val Ser Ser Lys		1090	1095	1100
Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu Val Ser Leu Arg Leu Asp		1105	1110	1115
Phe Leu Arg Ile Ile Cys Ser His Glu His Tyr Val Thr Leu Asn Leu		1125	1130	1135
Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser Pro Ser Pro Ser Val Ser		1140	1145	1150
Ser Ala Thr Ser Gln Ser Ser Gly Phe Ser Thr Asn Val Gln Asp Gln		1155	1160	1165
Lys Ile Ala Asn Met Phe Glu Leu Ser Val Pro Phe Arg Gln Gln His		1170	1175	1180
Tyr Leu Ala Gly Leu Val Leu Thr Glu Leu Ala Val Ile Leu Asp Pro		1185	1190	1195
Asp Ala Glu Gly Leu Phe Gly Leu His Lys Lys Val Ile Asn Met Val		1205	1210	1215
His Asn Leu Leu Ser Ser His Asp Ser Asp Pro Arg Tyr Ser Asp Pro		1220	1225	1230

Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu			
1265	1270	1275	1280
Ser Gly Ser Met Ile Ser Gln Thr Val Ala Met Ala Ile Ala Gly Thr			
1285	1290		1295
Ser Val Pro Gln Leu Thr Arg Pro Gly Ser Phe Leu Leu Thr Ser Thr			
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Ser Gly Arg Gln His Thr Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu			
1315	1320		1325
Leu Ile Cys Leu Leu Trp Val Leu Lys Asn Ala Asp Glu Thr Val Leu			
1330	1335		1340
Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu			
1345	1350	1355	1360
Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys			
1365	1370		1375
Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met			
1380	1385		1390
Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln			
1395	1400		1405
Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly			
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Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr			
1425	1430	1435	1440
His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile			
1445	1450		1455
Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu			
1460	1465		1470
Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr			
1475	1480		1485
Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His			
1490	1495		1500
Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala			
1505	1510	1515	1520
Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu			
1525	1530		1535
Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys			
1540	1545		1550

Lys Met Gln Val	Pro Met	Ser Leu Ser Ser Leu Val Gly Thr Ser Gln
1585	1590	1595 1600
Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr		
1605	1610	1615
Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln		
1620	1625	1630
Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val		
1635	1640	1645
Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met		
1650	1655	1660
Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp		
1665	1670	1675 1680
Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu		
1685	1690	1695
Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu		
1700	1705	1710
Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe		
1715	1720	1725
Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp		
1730	1735	1740
Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr		
1745	1750	1755 1760
Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser		
1765	1770	1775
Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile		
1780	1785	1790
Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His		
1795	1800	1805
Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly		
1810	1815	1820
Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr		
1825	1830	1835 1840
Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala		
1845	1850	1855
Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly		
1860	1865	1870

Tyr	Glu	Val	Asp	Glu	Glu	Val	Asp	Lys	Asp	Glu	Asp	Ala	Ala	Ser	Leu	85	90	95
Gly	Ser	Gln	Lys	Gly	Gly	Ile	Thr	Lys	His	Gly	Trp	Leu	Tyr	Lys	Gly	100	105	110
Asn	Met	Asn	Ser	Ala	Ile	Ser	Val	Thr	Met	Arg	Ser	Phe	Lys	Arg	Arg	115	120	125
Phe	Phe	His	Leu	Ile	Gln	Leu	Gly	Asp	Gly	Ser	Tyr	Asn	Leu	Asn	Phe	130	135	140
Tyr	Lys	Asp	Glu	Lys	Ile	Ser	Lys	Glu	Pro	Lys	Gly	Ser	Ile	Phe	Leu	145	150	155
Asp	Ser	Cys	Met	Gly	Val	Val	Gln	Asn	Asn	Lys	Val	Arg	Arg	Phe	Ala	165	170	175
Phe	Glu	Leu	Lys	Met	Gln	Asp	Lys	Ser	Ser	Tyr	Leu	Leu	Ala	Ala	Asp	180	185	190
Ser	Glu	Val	Glu	Met	Glu	Glu	Trp	Ile	Thr	Ile	Leu	Asn	Lys	Ile	Leu	195	200	205
Gln	Leu	Asn	Phe	Glu	Ala	Ala	Met	Gln	Glu	Lys	Arg	Asn	Gly	Asp	Ser	210	215	220
His	Glu	Asp	Asp	Glu	Gln	Ser	Lys	Leu	Glu	Gly	Ser	Gly	Ser	Gly	Leu	225	230	235
Asp	Ser	Tyr	Leu	Pro	Glu	Leu	Ala	Lys	Ser	Ala	Arg	Glu	Ala	Glu	Ile	245	250	255
Lys	Leu	Lys	Ser	Glu	Ser	Arg	Val	Lys	Leu	Phe	Tyr	Leu	Asp	Pro	Asp	260	265	270
Ala	Gln	Lys	Leu	Asp	Phe	Ser	Ser	Ala	Glu	Pro	Glu	Val	Lys	Ser	Phe	275	280	285
Glu	Glu	Lys	Phe	Gly	Lys	Arg	Ile	Leu	Val	Lys	Cys	Asn	Asp	Leu	Ser	290	295	300
Phe	Asn	Leu	Gln	Cys	Cys	Val	Ala	Glu	Asn	Glu	Glu	Gly	Pro	Thr	Thr	305	310	315
Asn	Val	Glu	Pro	Phe	Phe	Val	Thr	Leu	Ser	Leu	Phe	Asp	Ile	Lys	Tyr	325	330	335
Asn	Arg	Lys	Ile	Ser	Ala	Asp	Phe	His	Val	Asp	Leu	Asn	His	Phe	Ser	340	345	350
Val	Arg	Gln	Met	Leu	Ala	Thr	Thr	Ser	Pro	Ala	Leu	Met	Asn	Gly	Ser	355	360	365

Ile	Phe	Leu	Val	Ala	Arg	Ile	Glu	Lys	Val	Leu	Gln	Gly	Ser	Ile	Thr	405	410	415	
His	Cys	Ala	Glu	Pro	Tyr	Met	Lys	Ser	Ser	Asp	Ser	Ser	Lys	Val	Ala	420	425	430	
Gln	Lys	Val	Leu	Lys	Asn	Ala	Lys	Gln	Ala	Cys	Gln	Arg	Leu	Gly	Gln	435	440	445	
Tyr	Arg	Met	Pro	Phe	Ala	Trp	Ala	Ala	Arg	Thr	Leu	Phe	Lys	Asp	Ala	450	455	460	
Ser	Gly	Asn	Leu	Asp	Lys	Asn	Ala	Arg	Phe	Ser	Ala	Ile	Tyr	Arg	Gln	465	470	475	480
Asp	Ser	Asn	Lys	Leu	Ser	Asn	Asp	Asp	Met	Leu	Lys	Leu	Leu	Ala	Asp	485	490	495	
Phe	Arg	Lys	Pro	Glu	Lys	Met	Ala	Lys	Leu	Pro	Val	Ile	Leu	Gly	Asn	500	505	510	
Leu	Asp	Ile	Thr	Ile	Asp	Asn	Val	Ser	Ser	Asp	Phe	Pro	Asn	Tyr	Val	515	520	525	
Asn	Ser	Ser	Tyr	Ile	Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys	Thr	530	535	540	
Pro	Ile	Thr	Phe	Glu	Val	Glu	Glu	Phe	Val	Pro	Cys	Ile	Pro	Lys	His	545	550	555	560
Thr	Gln	Pro	Tyr	Thr	Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro	Lys	565	570	575	
Tyr	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Ser	Phe	Ala	Lys	Ala	Arg	Asn	Ile	580	585	590	
Ala	Ile	Cys	Ile	Glu	Phe	Lys	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Gln	Pro	595	600	605	
Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg	Ser	610	615	620	
Ala	Phe	Ala	Ala	Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr	Asp	625	630	635	640
Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His	Leu	645	650	655	
Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser	660	665	670	
Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu	675	680	685	

Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys
				725					730					735	
Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln
			740					745					750		
Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser
		755				760						765			
Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu
	770					775					780				
His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu
	785				790					795					800
Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala
			805						810					815	
Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu
			820				825						830		
Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys
		835					840					845			
Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu
	850					855					860				
Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr
	865				870					875					880
Ser	Asn	Lys	Leu	Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile
			885						890					895	
Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu
			900					905					910		
Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val
		915					920					925			
Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro
	930					935					940				
Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg
	945				950					955					960
Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn
			965					970						975	
Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr
			980					985					990		
Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro
		995				1000						1005			

Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu
 1045 1050 1055
 Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu
 1060 1065 1070
 Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala
 1075 1080 1085
 Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn
 1090 1095 1100
 Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala
 1105 1110 1115 1120
 Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro
 1125 1130 1135
 Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys
 1140 1145 1150
 Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser
 1155 1160 1165
 Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu
 1170 1175 1180
 Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys
 1185 1190 1195 1200
 Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser
 1205 1210 1215
 Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu
 1220 1225 1230
 Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe
 1235 1240 1245
 Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr
 1250 1255 1260
 Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr
 1265 1270 1275 1280
 Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys
 1285 1290 1295
 Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala
 1300 1305 1310
 Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His
 1315 1320 1325

Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His	1365	1370	1375
Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln	1380	1385	1390
Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg	1395	1400	1405
Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp	1410	1415	1420
Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys	1425	1430	1435
Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met	1445	1450	1455
Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His	1460	1465	1470
Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly	1475	1480	1485
Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys	1490	1495	1500
Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val	1505	1510	1515
Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln	1525	1530	1535
Met Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr	1540	1545	1550
Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp	1555	1560	1565
Leu Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu	1570	1575	1580
Ala Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu	1585	1590	1595
Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile	1605	1610	1615
Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met	1620	1625	1630
Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln	1635	1640	1645

Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr
 1685 1690 1695
 Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys
 1700 1705 1710
 Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn
 1715 1720 1725
 Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val
 1730 1735 1740
 Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe
 1745 1750 1755 1760
 Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr
 1765 1770 1775
 Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg
 1780 1785 1790
 Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile
 1795 1800 1805
 Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala
 1810 1815 1820
 Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser
 1825 1830 1835 1840
 Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser
 1845 1850 1855
 Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe
 1860 1865 1870
 Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu
 1875 1880 1885
 Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu
 1890 1895 1900
 Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu
 1905 1910 1915 1920
 Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile
 1925 1930 1935
 Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro
 1940 1945 1950
 Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr
 1955 1960 1965

<210> 92

<211> 2045

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-7

<400> 92

Met	Ala	Ala	Ser	Glu	Arg	Arg	Ala	Phe	Ala	His	Lys	Ile	Asn	Arg	Thr
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Val	Ala	Ala	Glu	Val	Arg	Lys	Gln	Val	Ser	Arg	Glu	Arg	Ser	Gly	Ser
			20				25						30		
Pro	His	Ser	Ser	Arg	Arg	Cys	Ser	Ser	Ser	Leu	Gly	Val	Pro	Leu	Thr
		35				40						45			
Glu	Val	Val	Glu	Pro	Leu	Asp	Phe	Glu	Asp	Val	Leu	Leu	Ser	Arg	Pro
	50					55					60				
Pro	Asp	Ala	Glu	Pro	Gly	Pro	Leu	Arg	Asp	Leu	Val	Glu	Phe	Pro	Ala
	65				70					75				80	
Asp	Asp	Leu	Glu	Leu	Leu	Leu	Gln	Pro	Arg	Glu	Cys	Arg	Thr	Thr	Glu
			85						90					95	
Pro	Gly	Ile	Pro	Lys	Asp	Glu	Lys	Leu	Asp	Ala	Gln	Val	Arg	Ala	Ala
			100					105						110	
Val	Glu	Met	Tyr	Ile	Glu	Asp	Trp	Val	Ile	Val	His	Arg	Arg	Tyr	Gln
		115					120						125		
Tyr	Leu	Ser	Ala	Ala	Tyr	Ser	Pro	Val	Thr	Thr	Asp	Thr	Gln	Arg	Glu
	130					135						140			
Arg	Gln	Lys	Gly	Leu	Pro	Arg	Gln	Val	Phe	Glu	Gln	Asp	Ala	Ser	Gly
	145				150					155					160
Asp	Glu	Arg	Ser	Gly	Pro	Glu	Asp	Ser	Asn	Asp	Ser	Arg	Arg	Gly	Ser
				165					170					175	
Gly	Ser	Pro	Glu	Asp	Thr	Pro	Arg	Ser	Ser	Gly	Ala	Ser	Ser	Ile	Phe
			180					185						190	
Asp	Leu	Arg	Asn	Leu	Ala	Ala	Asp	Ser	Leu	Leu	Pro	Ser	Leu	Leu	Glu
		195					200					205			
Arg	Ala	Ala	Pro	Glu	Asp	Val	Asp	Arg	Arg	Asn	Glu	Thr	Leu	Arg	Arg
	210				215						220				
Gln	His	Arg	Pro	Pro	Ala	Leu	Leu	Thr	Leu	Tyr	Pro	Ala	Pro	Asp	Glu
	225				230					235				240	

Glu	Ile	Glu	Pro	Ile	Phe	Gly	Ile	Leu	Ala	Leu	Tyr	Asp	Val	Arg	Glu	
275						280						285				
Lys	Lys	Lys	Ile	Ser		Glu	Asn	Phe	Tyr	Phe	Asp	Leu	Asn	Ser	Asp	Ser
290						295						300				
Met	Lys	Gly	Leu	Leu	Arg	Ala	His	Gly	Thr	His	Pro	Ala	Ile	Ser	Thr	
305						310						315			320	
Leu	Ala	Arg	Ser	Ala	Ile	Phe	Ser	Val	Thr	Tyr	Pro	Ser	Pro	Asp	Ile	
			325						330						335	
Phe	Leu	Val	Ile	Lys	Leu	Glu	Lys	Val	Leu	Gln	Gln	Gly	Asp	Ile	Ser	
			340						345						350	
Glu	Cys	Cys	Glu	Pro	Tyr	Met	Val	Leu	Lys	Glu	Val	Asp	Thr	Ala	Lys	
			355						360						365	
Asn	Lys	Glu	Lys	Leu	Glu	Lys	Leu	Arg	Leu	Ala	Ala	Glu	Gln	Phe	Cys	
370						375						380				
Thr	Arg	Leu	Gly	Arg	Tyr	Arg	Met	Pro	Phe	Ala	Trp	Thr	Ala	Val	His	
385						390						395			400	
Leu	Ala	Asn	Ile	Val	Ser	Ser	Ala	Gly	Gln	Leu	Asp	Arg	Asp	Ser	Asp	
			405						410						415	
Ser	Glu	Gly	Glu	Arg	Arg	Pro	Ala	Trp	Thr	Asp	Arg	Arg	Arg	Arg	Gly	
			420						425						430	
Pro	Gln	Asp	Arg	Ala	Ser	Ser	Gly	Asp	Asp	Ala	Cys	Ser	Phe	Ser	Gly	
			435						440						445	
Phe	Arg	Pro	Ala	Thr	Leu	Thr	Val	Thr	Asn	Phe	Phe	Lys	Gln	Glu	Ala	
450						455						460				
Glu	Arg	Leu	Ser	Asp	Glu	Asp	Leu	Phe	Lys	Phe	Leu	Ala	Asp	Met	Arg	
465						470						475			480	
Arg	Pro	Ser	Ser	Leu	Leu	Arg	Arg	Leu	Arg	Pro	Val	Thr	Ala	Gln	Leu	
			485						490						495	
Lys	Ile	Asp	Ile	Ser	Pro	Ala	Pro	Glu	Asn	Pro	His	Phe	Cys	Leu	Ser	
			500						505						510	
Pro	Glu	Leu	His	Ile	Lys	Pro	Tyr	Pro	Asp	Pro	Arg	Gly	Arg	Pro		
515						520						525				
Thr	Lys	Glu	Ile	Leu	Glu	Phe	Pro	Ala	Arg	Glu	Val	Tyr	Ala	Pro	His	
530						535						540				
Thr	Ser	Tyr	Arg	Asn	Leu	Gly	Tyr	Val	Tyr	Pro	His	Ser	Leu	Asn	Phe	
545						550						555			560	

Ser	Ser	Cys	Ser	Glu	Phe	Thr	Arg	Glu	Ala	Phe	Thr	Pro	Val	Val	Tyr
		595					600					605			
His	Asn	Lys	Ser	Pro	Glu	Phe	Tyr	Glu	Glu	Phe	Lys	Leu	His	Leu	Pro
	610					615					620				
Ala	Cys	Val	Thr	Glu	Asn	His	His	Leu	Leu	Phe	Thr	Phe	Tyr	His	Val
625					630					635					640
Ser	Cys	Gln	Pro	Arg	Pro	Gly	Thr	Ala	Leu	Glu	Thr	Pro	Val	Gly	Phe
				645					650					655	
Thr	Trp	Ile	Pro	Leu	Leu	Gln	His	Gly	Arg	Leu	Arg	Thr	Gly	Pro	Phe
			660					665					670		
Cys	Leu	Pro	Val	Ser	Val	Asp	Gln	Pro	Pro	Pro	Ser	Tyr	Ser	Val	Leu
		675					680					685			
Thr	Pro	Asp	Val	Ala	Leu	Pro	Gly	Met	Arg	Trp	Val	Asp	Gly	His	Lys
	690					695					700				
Gly	Val	Phe	Ser	Val	Glu	Leu	Thr	Ala	Val	Ser	Ser	Val	His	Pro	Gln
705					710					715					720
Asp	Pro	Tyr	Leu	Asp	Lys	Phe	Phe	Thr	Leu	Val	His	Val	Leu	Glu	Glu
			725						730					735	
Gly	Ala	Phe	Pro	Phe	Arg	Leu	Lys	Asp	Thr	Val	Leu	Ser	Glu	Gly	Asn
			740					745					750		
Val	Glu	Gln	Glu	Leu	Arg	Ala	Ser	Leu	Ala	Ala	Leu	Arg	Leu	Ala	Ser
		755					760					765			
Pro	Glu	Pro	Leu	Val	Ala	Phe	Ser	His	His	Val	Leu	Asp	Lys	Leu	Val
	770					775					780				
Arg	Leu	Val	Ile	Arg	Pro	Pro	Ile	Ile	Ser	Gly	Gln	Ile	Val	Asn	Leu
785				790						795					800
Gly	Arg	Gly	Ala	Phe	Glu	Ala	Met	Ala	His	Val	Val	Ser	Leu	Val	His
			805						810					815	
Arg	Ser	Leu	Glu	Ala	Ala	Gln	Asp	Ala	Arg	Gly	His	Cys	Pro	Gln	Leu
			820				825						830		
Ala	Ala	Tyr	Val	His	Tyr	Ala	Phe	Arg	Leu	Pro	Gly	Thr	Glu	Pro	Ser
		835					840					845			
Leu	Pro	Asp	Gly	Ala	Pro	Pro	Val	Thr	Val	Gln	Ala	Ala	Thr	Leu	Ala
	850					855					860				
Arg	Gly	Ser	Gly	Arg	Pro	Ala	Ser	Leu	Tyr	Leu	Ala	Arg	Ser	Lys	Ser
865					870					875					880

Ala Leu Gln Trp Val Val Ser Ser Ser Ala Val Arg Glu Ala Ile Leu	915	920	925
Gln His Ala Trp Phe Phe Phe Gln Leu Met Val Lys Ser Met Ala Leu	930	935	940
His Leu Leu Leu Gly Gln Arg Leu Asp Thr Pro Arg Lys Leu Arg Phe	945	950	955
Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly Ser Val Gly	965	970	975
Leu Glu Val Ile Thr Arg Val His Lys Asp Val Glu Leu Ala Glu His	980	985	990
Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu Ser Leu Val	995	1000	1005
Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr Lys Gln Val	1010	1015	1020
Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu Leu Thr Leu	1025	1030	1035
Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His Tyr Val Thr	1045	1050	1055
Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser Pro Ser Pro	1060	1065	1070
Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser Ser Gln Ala	1075	1080	1085
Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly Pro Phe Arg	1090	1095	1100
Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu Ala Leu Ala	1105	1110	1115
Leu Gln Glu Asp Gln Asp Val Arg His Leu Ala Leu Ala Val Leu Lys	1125	1130	1135
Asn Leu Met Ala Lys His Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg	1140	1145	1150
Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met Pro Leu Tyr Gly Met Leu	1155	1160	1165
Leu Asp Asn Met Pro Arg Ile Arg Leu His Asp Phe Ala Glu Gly Pro	1170	1175	1180
Gly Gln Arg Ser Arg Leu Ala Ser Met Leu Asp Ser Asp Thr Glu Gly	1185	1190	1195
			1200

Pro	Pro	Thr	Ala	Ser	Arg	Ala	Gly	Cys	Ala	Leu	Ser	Ala	Glu	Ser	Ser	1235	1240	1245
Arg	Thr	Leu	Leu	Ala	Cys	Val	Leu	Trp	Val	Leu	Lys	Asn	Thr	Glu	Pro	1250	1255	1260
Ala	Leu	Leu	Gln	Arg	Trp	Ala	Thr	Asp	Leu	Thr	Leu	Pro	Gln	Leu	Gly	1265	1270	1275 1280
Arg	Leu	Leu	Asp	Leu	Leu	Tyr	Leu	Cys	Leu	Ala	Ala	Phe	Glu	Tyr	Lys	1285	1290	1295
Gly	Lys	Lys	Ala	Phe	Glu	Arg	Ile	Asn	Ser	Leu	Thr	Phe	Lys	Lys	Ser	1300	1305	1310
Leu	Asp	Met	Lys	Ala	Arg	Leu	Glu	Glu	Ala	Ile	Leu	Gly	Thr	Ile	Gly	1315	1320	1325
Ala	Arg	Gln	Glu	Met	Val	Arg	Arg	Ser	Arg	Glu	Arg	Ser	Pro	Phe	Gly	1330	1335	1340
Asn	Pro	Glu	Asn	Val	Arg	Trp	Arg	Lys	Ser	Val	Thr	His	Trp	Lys	Gln	1345	1350	1355 1360
Thr	Ser	Asp	Arg	Val	Asp	Lys	Thr	Lys	Asp	Glu	Met	Glu	His	Glu	Ala	1365	1370	1375
Leu	Val	Glu	Gly	Asn	Leu	Ala	Thr	Glu	Ala	Ser	Leu	Val	Val	Leu	Asp	1380	1385	1390
Thr	Leu	Glu	Ile	Ile	Val	Gln	Thr	Val	Met	Leu	Ser	Glu	Ala	Arg	Glu	1395	1400	1405
Ser	Val	Leu	Gly	Ala	Val	Leu	Lys	Val	Val	Leu	Tyr	Ser	Leu	Gly	Ser	1410	1415	1420
Ala	Gln	Ser	Ala	Leu	Phe	Leu	Gln	His	Gly	Leu	Ala	Thr	Gln	Arg	Ala	1425	1430	1435 1440
Leu	Val	Ser	Lys	Phe	Pro	Glu	Leu	Leu	Phe	Glu	Glu	Asp	Thr	Glu	Leu	1445	1450	1455
Cys	Ala	Asp	Leu	Cys	Leu	Arg	Leu	Leu	Arg	His	Cys	Gly	Ser	Arg	Ile	1460	1465	1470
Ser	Thr	Ile	Arg	Thr	His	Ala	Ser	Ala	Ser	Leu	Tyr	Leu	Leu	Met	Arg	1475	1480	1485
Gln	Asn	Phe	Glu	Ile	Gly	His	Asn	Phe	Ala	Arg	Val	Lys	Met	Gln	Val	1490	1495	1500
Thr	Met	Ser	Leu	Ser	Ser	Leu	Val	Gly	Thr	Gln	Asn	Phe	Ser	Glu		1505	1510	1515 1520

Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met Lys Glu	1555	1560	1565
His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala	1570	1575	1580
Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn	1585	1590	1595
Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala Ala Gln	1605	1610	1615
Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala Leu Leu	1620	1625	1630
Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln Asn Ile	1635	1640	1645
Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile Leu Ser	1650	1655	1660
Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu Leu Gly	1665	1670	1675
Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met Gly Gly	1685	1690	1695
Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro Ile Leu	1700	1705	1710
Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly Lys Leu	1715	1720	1725
Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp Glu Arg	1730	1735	1740
Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His Phe Gly	1745	1750	1755
Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile Thr Lys	1765	1770	1775
Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu Arg Phe	1780	1785	1790
Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val Asp Lys	1795	1800	1805
Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu	1810	1815	1820
Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr Phe Asp	1825	1830	1835
			1840

Lys	Ala	Glu	Asn	Leu	Leu	Val	Lys	Glu	Ala	Cys	Lys	Phe	Tyr	Ser	Ser	100	105	110
Gln	Trp	His	Val	Val	Asn	Tyr	Lys	Tyr	Glu	Gln	Tyr	Ser	Gly	Asp	Ile	115	120	125
Arg	Gln	Leu	Pro	Arg	Ala	Glu	Tyr	Lys	Pro	Glu	Lys	Leu	Pro	Ser	His	130	135	140
Ser	Phe	Glu	Ile	Asp	His	Glu	Asp	Ala	Asp	Lys	Asp	Glu	Asp	Thr	Thr	145	150	155
Ser	His	Ser	Ser	Ser	Lys	Gly	Gly	Gly	Gly	Ala	Gly	Gly	Thr	Gly	Val	165	170	175
Phe	Lys	Ser	Gly	Trp	Leu	Tyr	Lys	Gly	Asn	Phe	Asn	Ser	Thr	Val	Asn	180	185	190
Asn	Thr	Val	Thr	Val	Arg	Ser	Phe	Lys	Lys	Arg	Tyr	Phe	Gln	Leu	Thr	195	200	205
Gln	Leu	Pro	Asp	Asn	Ser	Tyr	Ile	Met	Asn	Phe	Tyr	Lys	Asp	Glu	Lys	210	215	220
Ile	Ser	Lys	Glu	Pro	Lys	Gly	Cys	Ile	Phe	Leu	Asp	Ser	Cys	Thr	Gly	225	230	235
Val	Val	Gln	Asn	Asn	Arg	Leu	Arg	Lys	Tyr	Ala	Phe	Glu	Leu	Lys	Met	245	250	255
Asn	Asp	Leu	Thr	Tyr	Phe	Val	Leu	Ala	Ala	Glu	Thr	Glu	Ser	Asp	Met	260	265	270
Asp	Glu	Trp	Ile	His	Thr	Leu	Asn	Arg	Ile	Leu	Gln	Ile	Ser	Pro	Glu	275	280	285
Gly	Pro	Leu	Gln	Gly	Arg	Arg	Ser	Thr	Glu	Leu	Thr	Asp	Leu	Gly	Leu	290	295	300
Asp	Ser	Leu	Asp	Asn	Ser	Val	Thr	Cys	Glu	Cys	Thr	Pro	Glu	Glu	Thr	305	310	315
Asp	Ser	Ser	Glu	Asn	Asn	Leu	His	Ala	Asp	Phe	Ala	Lys	Tyr	Leu	Thr	325	330	335
Glu	Thr	Glu	Asp	Thr	Val	Lys	Thr	Thr	Arg	Asn	Met	Glu	Arg	Leu	Asn	340	345	350
Leu	Phe	Ser	Leu	Asp	Pro	Asp	Ile	Asp	Thr	Leu	Lys	Leu	Gln	Lys	Lys	355	360	365
Asp	Leu	Leu	Glu	Pro	Glu	Ser	Val	Ile	Lys	Pro	Phe	Glu	Glu	Lys	Ala	370	375	380

Phe	Phe	Val	Ser	Val	Ala	Leu	Tyr	Asp	Leu	Arg	Asp	Ser	Arg	Lys	Ile	420	425	430
Ser	Ala	Asp	Phe	His	Val	Asp	Leu	Asn	His	Ala	Ala	Val	Arg	Gln	Met	435	440	445
Leu	Leu	Gly	Ala	Ser	Val	Ala	Leu	Glu	Asn	Gly	Asn	Ile	Asp	Thr	Ile	450	455	460
Thr	Pro	Arg	Gln	Ser	Glu	Glu	Pro	His	Ile	Lys	Gly	Leu	Pro	Glu	Glu	465	470	475
Trp	Leu	Lys	Phe	Pro	Lys	Gln	Ala	Val	Phe	Ser	Val	Ser	Asn	Pro	His	485	490	495
Ser	Glu	Ile	Val	Leu	Val	Ala	Lys	Ile	Glu	Lys	Val	Leu	Met	Gly	Asn	500	505	510
Ile	Ala	Ser	Gly	Ala	Glu	Pro	Tyr	Ile	Lys	Asn	Pro	Asp	Ser	Asn	Lys	515	520	525
Tyr	Ala	Gln	Lys	Ile	Leu	Lys	Ser	Asn	Arg	Gln	Phe	Cys	Ser	Lys	Leu	530	535	540
Gly	Lys	Tyr	Arg	Arg	Ala	Phe	Ala	Trp	Ala	Val	Arg	Ser	Val	Phe	Lys	545	550	555
Asp	Asn	Gln	Gly	Asn	Val	Asp	Arg	Asp	Ser	Arg	Phe	Ser	Pro	Leu	Phe	565	570	575
Arg	Gln	Glu	Ser	Ser	Lys	Ile	Ser	Thr	Glu	Asp	Leu	Val	Lys	Leu	Val	580	585	590
Ser	Asp	Tyr	Arg	Arg	Ala	Asp	Arg	Ile	Ser	Lys	Met	Gln	Thr	Ile	Pro	595	600	605
Gly	Ser	Leu	Asp	Ile	Ala	Val	Asp	Asn	Val	Pro	Leu	Glu	His	Pro	Asn	610	615	620
Cys	Val	Thr	Ser	Ser	Phe	Ile	Pro	Val	Lys	Pro	Phe	Asn	Met	Met	Ala	625	630	635
Gln	Thr	Glu	Pro	Thr	Val	Glu	Val	Glu	Glu	Phe	Val	Tyr	Asp	Ser	Thr	645	650	655
Lys	Tyr	Cys	Arg	Pro	Tyr	Arg	Val	Tyr	Lys	Asn	Gln	Ile	Tyr	Ile	Tyr	660	665	670
Pro	Lys	His	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Cys	Phe	Asn	Lys	Ala	Arg	675	680	685
Asn	Ile	Thr	Val	Cys	Ile	Glu	Phe	Lys	Asn	Ser	Asp	Glu	Glu	Ser	Ala	690	695	700

Ser	Asp	Glu	Val	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	
			740					745					750			
His	Ile	Leu	Phe	Ser	Phe	Tyr	His	Val	Thr	Cys	Asp	Ile	Asn	Ala	Lys	
		755					760					765				
Ala	Asn	Ala	Lys	Lys	Lys	Glu	Ala	Leu	Glu	Thr	Ser	Val	Gly	Tyr	Ala	
	770				775						780					
Trp	Leu	Pro	Leu	Met	Lys	His	Asp	Gln	Ile	Ala	Ser	Gln	Glu	Tyr	Asn	
785					790					795					800	
Ile	Pro	Ile	Ala	Thr	Ser	Leu	Pro	Pro	Asn	Tyr	Leu	Ser	Phe	Gln	Asp	
				805					810					815		
Ser	Ala	Ser	Gly	Lys	His	Gly	Gly	Ser	Asp	Ile	Lys	Trp	Val	Asp	Gly	
			820					825					830			
Gly	Lys	Pro	Leu	Phe	Lys	Val	Ser	Thr	Phe	Val	Val	Ser	Thr	Val	Asn	
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Thr	Gln	Asp	Pro	His	Val	Asn	Ala	Phe	Phe	Gln	Glu	Cys	Gln	Lys	Arg	
	850					855					860					
Glu	Lys	Asp	Met	Ser	Gln	Ser	Pro	Thr	Ser	Asn	Phe	Ile	Arg	Ser	Cys	
865					870					875					880	
Lys	Asn	Leu	Leu	Asn	Val	Glu	Lys	Ile	His	Ala	Ile	Met	Ser	Phe	Leu	
				885					890					895		
Pro	Ile	Ile	Leu	Asn	Gln	Leu	Phe	Lys	Val	Leu	Val	Gln	Asn	Glu	Glu	
			900					905					910			
Asp	Glu	Ile	Thr	Thr	Thr	Val	Thr	Arg	Val	Leu	Pro	Asp	Ile	Val	Ala	
		915					920					925				
Lys	Cys	His	Glu	Glu	Gln	Leu	Asp	His	Ser	Val	Gln	Ser	Tyr	Ile	Lys	
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Phe	Val	Phe	Lys	Thr	Arg	Ala	Cys	Lys	Glu	Arg	Pro	Val	His	Glu	Asp	
945					950					955					960	
Leu	Ala	Lys	Asn	Val	Thr	Gly	Leu	Leu	Lys	Ser	Asn	Asp	Ser	Pro	Thr	
				965					970					975		
Val	Lys	His	Val	Leu	Lys	His	Ser	Trp	Phe	Phe	Phe	Ala	Ile	Ile	Leu	
			980					985					990			
Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Asp	Thr	Asn	Lys	Ile	Gln	Leu	Pro	
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Arg	Pro	Gln	Arg	Phe	Pro	Glu	Ser	Tyr	Gln	Asn	Glu	Leu	Asp	Asn	Leu	
	1010					1015					1020					

Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys Met Val Asn Asn	1060	1065	1070
Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr Leu Cys Gln Tyr	1075	1080	1085
Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu His Phe Ile Pro	1090	1095	1100
Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp Pro Leu Thr Pro	1105	1110	1115 1120
Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met Pro Glu Tyr Ser	1125	1130	1135
Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile Gly Ile Leu Leu	1140	1145	1150
Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp Val Arg His Leu	1155	1160	1165
Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His Ser Phe Asp Asp	1170	1175	1180
Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met	1185	1190	1195 1200
Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg Ile Tyr Leu Lys	1205	1210	1215
Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln Gly Ser Arg Asp	1220	1225	1230
Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr Ala Ile Lys His	1235	1240	1245
Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val Leu Asn Ser Ile	1250	1255	1260
Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn His Ala Asp Ser	1265	1270	1275 1280
Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser Thr Asn Glu Lys	1285	1290	1295
Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro Arg Pro Leu Ala	1300	1305	1310
Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp Gln Ala Glu Thr	1315	1320	1325
Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys Thr Ile Ser Tyr	1330	1335	1340

Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala Phe Lys Phe Val
 1380 1385 1390
 Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser Asn Pro Ser Cys
 1395 1400 1405
 Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser Thr Ser Arg His
 1410 1415 1420
 Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro Ile Ile Arg Gly
 1425 1430 1435 1440
 Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met Leu Asp Asn Thr
 1445 1450 1455
 Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His His Val Asp Thr
 1460 1465 1470
 Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile Leu Asp Leu Val
 1475 1480 1485
 Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln Gln Cys Asp Cys
 1490 1495 1500
 Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr Met Leu Phe Phe
 1505 1510 1515 1520
 Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val Phe Ala Ser Leu
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 Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe Gln Gly Pro Ala
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 Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys Cys Cys Asn His
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 1570 1575 1580
 Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser Ile Val Arg Ser
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 His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile Ala Asp Ala Gly
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 Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile Thr Asn Asn Phe
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 Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe Pro Ala Glu Val
 1635 1640 1645
 Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
 1650 1655 1660

Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly Asp Leu Ser Glu
 1700 1705 1710

Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile Ala Glu Tyr Leu
 1715 1720 1725

Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys Thr Ala Ser Leu
 1730 1735 1740

Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser Leu Leu Thr Thr
 1745 1750 1755 1760

Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro Ala Phe Leu Ser
 1765 1770 1775

Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys Glu Asp Ser Gly
 1780 1785 1790

Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr
 1795 1800 1805

Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr Glu Leu Ile Ala
 1810 1815 1820

Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys Gln Arg Asp Phe
 1825 1830 1835 1840

Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg Ser Tyr Leu Lys
 1845 1850 1855

Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe Gly Arg Tyr Tyr
 1860 1865 1870

Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Gly Lys
 1875 1880 1885

Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser
 1890 1895 1900

Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val
 1905 1910 1915 1920

Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys Asp Leu Asp Pro
 1925 1930 1935

Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Glu
 1940 1945 1950

Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met His His Asn Ile
 1955 1960 1965

Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His
 1970 1975 1980

Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Arg
 2020 2025 2030
 Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu Glu Val Asp Met
 2035 2040 2045
 Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn
 2050 2055 2060
 Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala
 2065 2070 2075 2080
 Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg
 2085 2090 2095
 Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val Asn Glu Arg Leu
 2100 2105 2110
 Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr
 2115 2120 2125
 Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn Glu Gln Ile Thr
 2130 2135 2140
 Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln Thr Cys Thr Arg
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motif E

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Ile or Leu

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Asp, Glu or Gln

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Met, Ile, Leu or Val

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Pro Xaa Glu Xaa Ala Ile Xaa Xaa Xaa
1 5

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conserved non-tyrosine containing region from
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Gln or Asn

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28

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29

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HC7gS5

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22

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HC7gS3

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23

11 Artificial Sequence

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